

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:38:20 ; Search time 88.9271 Seconds  
(without alignments)  
1488.535 Million cell updates/sec

Title: US-10-070-532-4

Perfect score: 1937

Sequence: 1 MEPSATPGAQMGVPPGSREP.....NSAANPIIYNFLSGLPWSLL 369

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:  
1: geneseqp1980s:  
2: geneseqp1990s:  
3: geneseqp2000s:  
4: geneseqp2001s:  
5: geneseqp2002s:  
6: geneseqp2003as:  
7: geneseqp2003bs:  
8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query			Description
		Match	Length	DB ID	
1	1937	100.0	369	4 AAU00439	Aau00439 Human neu
2	1909	98.6	369	2 AAW06125	Aaw06125 Neuropept
3	1884	97.3	402	2 AAW06124	Aaw06124 Neuropept
4	1875	96.8	372	4 AAU00440	Aau00440 Human neu
5	1875	96.8	389	2 AAW80805	Aaw80805 Amino aci
6	1875	96.8	389	4 AAU11187	Aau11187 Human G p
7	1875	96.8	389	5 ABB08208	Abb08208 G-protein
8	1875	96.8	425	2 AAW80456	Aaw80456 G-protein
9	1875	96.8	425	4 AAU11188	Aau11188 Human G p

10	1875	96.8	425	4	AAU11186	Aau11186 Human G p
11	1875	96.8	425	4	AAB67079	Aab67079 Human HFG
12	1875	96.8	425	5	AAG78345	Aag78345 Human HFG
13	1875	96.8	425	6	ABP81941	Abp81941 Human ore
14	1875	96.8	425	7	ABG75058	Abg75058 Human ore
15	1875	96.8	425	7	ADK52564	Adk52564 Hematolog
16	1875	96.8	425	8	ADL22443	Adl22443 Human ore
17	1875	96.8	425	8	ADL22428	Adl22428 Human ore
18	1875	96.8	425	8	ADO29106	Ado29106 Human nov
19	1872	96.6	377	2	AAW06126	Aaw06126 Neuropept
20	1870	96.5	425	4	ABB56378	Abb56378 Non-endog
21	1869	96.5	425	4	AAU00438	Aau00438 Human neu
22	1869	96.5	425	4	AAB67489	Aab67489 Amino aci
23	1858.5	95.9	401	5	AAG78346	Aag78346 Human HFG
24	1842	95.1	425	4	AAE04740	Aae04740 Cynomolgo
25	1782	92.0	364	4	AAU00442	Aau00442 Human neu
26	1757	90.7	416	8	ADO29107	Ado29107 Mouse nov
27	1755	90.6	427	4	AAB47300	Aab47300 Dog orexi
28	1326.5	68.5	460	4	AAB61970	Aab61970 Rat HCRT
29	1326.5	68.5	460	6	ABG73515	Abg73515 Rat OX2R
30	1319.5	68.1	444	4	AAB61968	Aab61968 Canine wi
31	1316.5	68.0	444	4	AAB84416	Aab84416 Amino aci
32	1315.5	67.9	443	8	ADO29110	Ado29110 Mouse nov
33	1313.5	67.8	444	4	AAB98007	Aab98007 Human hyp
34	1313.5	67.8	444	4	AAB61969	Aab61969 Human HCR
35	1313.5	67.8	444	6	ABG73514	Abg73514 Human OX2
36	1313.5	67.8	444	6	ABP81942	Abp81942 Human ore
37	1313.5	67.8	444	7	ABG75059	Abg75059 Human ore
38	1313.5	67.8	444	8	ADO29109	Ado29109 Human nov
39	1312.5	67.8	444	2	AAY03649	Aay03649 Human 7-t
40	1308.5	67.6	444	4	ABB56379	Abb56379 Non-endog
41	1279	66.0	263	2	AAR91233	Aar91233 Rabbit G-
42	1279	66.0	263	2	AAW11236	Aaw11236 G-protein
43	1133.5	58.5	330	4	AAB61971	Aab61971 Canine na
44	966	49.9	327	4	AAB61972	Aab61972 Canine na
45	499.5	25.8	430	8	ADJ87508	Adj87508 Murine re

## ALIGNMENTS

### RESULT 1

AAU00439

ID AAU00439 standard; protein; 369 AA.

XX

AC AAU00439;

XX

DT 17-MAY-2001 (first entry)

XX

DE Human neuropeptide receptor splice variant 1.

XX

KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;  
KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;  
KW cardiovascular disorder; autoimmune disorder; infectious disorder;  
KW eating behaviour disorder; narcolepsy; neurological disease;  
KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;  
KW protein co-ordinate data.

XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 47. .72  
FT /label= TM1  
FT /note= "Transmembrane region 1"  
FT Region 83. .106  
FT /label= TM2  
FT /note= "Transmembrane region 2"  
FT Region 112. .142  
FT /label= TM3  
FT /note= "Transmembrane region 3"  
FT Region 163. .189  
FT /label= TM4  
FT /note= "Transmembrane region 4"  
FT Region 214. .239  
FT /label= TM5  
FT /note= "Transmembrane region 5"  
FT Region 299. .327  
FT /label= TM6  
FT /note= "Transmembrane region 6"  
FT Region 335. .363  
FT /label= TM7  
FT /note= "Transmembrane region 7"  
XX  
PN WO200117532-A1.  
XX  
PD 15-MAR-2001.  
XX  
PF 07-SEP-2000; 2000WO-US024518.  
XX  
PR 10-SEP-1999; 99US-00393696.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Soppet DR, Li Y, Rosen CA;  
XX  
DR WPI; 2001-183276/18.  
DR N-PSDB; AAS00492.  
XX  
PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,  
PT useful for preventing, treating or ameliorating obesity, narcolepsy,  
PT neurological disease and addiction to narcotics, nicotine and alcohol.  
XX  
PS Claim 3; Fig 5; 385pp; English.  
XX  
CC The present sequence represents human neuropeptide receptor splice  
CC variant 1. Two splice variants (AAU00439-AAU00440) and a possible mutant  
CC (AAU00442) of a novel human neuropeptide receptor (AAU00438) are  
CC described. The neuropeptide receptor shows sequence homology to the  
CC neuropeptide Y receptor. Polypeptides and polynucleotides of the  
CC neuropeptide receptor are useful for diagnosing, preventing, or treating  
CC a pathological condition in a subject related to the central nervous and  
CC peripheral nervous systems (CNS and PNS). The polypeptides and  
CC polynucleotides may be used to treat hyperproliferative, cardiovascular,  
CC autoimmune, nervous system or infectious disorders e.g. cancer, heart

CC disease, rheumatoid arthritis, Alzheimer's disease, HIV infection and  
CC diabetes mellitus. In particular they are useful for preventing, treating  
CC or ameliorating a medical condition in a mammal such as obesity/eating  
CC behaviour disorders, narcolepsy, neurological disease, addiction to  
CC narcotics, nicotine and alcohol, chronic pain, acute pain, migraine  
CC headaches and anxiety disorders. The polynucleotides encoding the  
CC neuropeptide receptor can also be used in gene therapy methods for  
CC treating such diseases

XX

SQ Sequence 369 AA;

Query Match 100.0%; Score 1937; DB 4; Length 369;  
Best Local Similarity 100.0%; Pred. No. 1.9e-189;  
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 KLWGRQIPGTTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSGLPWSLL 369  
||| ||| |||

Db 361 LSGLPWSLL 369

## RESULT 2

AAW06125

ID AAW06125 standard; protein; 369 AA.

XX

AC AAW06125;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor splice variant-1.

XX

KW Human; neuropeptide receptor; splice variant; drug screening;  
KW receptor-agonist; receptor-antagonist; anorectic; antitumour;  
KW anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;

KW sedative; diagnostic; gene therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 47. .72

FT /note= "Transmembrane region-1"

FT Domain 83. .106

FT /note= "Transmembrane region-2"

FT Domain 112. .142

FT /note= "Transmembrane region-3"

FT Domain 163. .189

FT /note= "Transmembrane region-4"

FT Domain 214. .239

FT /note= "Transmembrane region-5"

FT Domain 299. .327

FT /note= "Transmembrane region-6"

FT Domain 335. .363

FT /note= "Transmembrane region-7"

XX

PN WO9634877-A1.

XX

PD 07-NOV-1996.

XX

PF 05-MAY-1995; 95WO-US005616.

XX

PR 05-MAY-1995; 95WO-US005616.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Soppet DR, Li Y, Rosen CA;

XX

DR WPI; 1996-506094/50.

DR N-PSDB; AAT42827.

XX

PT Human neuro-peptide receptor polypeptide(s) - used to identify  
PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of  
PT obesity, Alzheimer's disease, epilepsy, etc.

XX

PS Disclosure; Page 51-52; 77pp; English.

XX

CC The sequence represents human adult hypothalamus neuropeptide receptor  
CC splice variant-1, which retains activity corresponding to the mature  
CC receptor (AAW06124), which is structurally related to the G-protein-  
CC coupled receptor family. The receptor variant contains 7 transmembrane  
CC regions. The receptor may be produced in recombinant form and used in a  
CC drug screening assay for isolation of receptor-agonists and -antagonists,  
CC which may be used as anorectic, antitumour, anticholesterolemic,  
CC neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The  
CC encoding DNA may be used in genetic disease diagnosis or gene therapy.  
CC The receptor itself and its corresponding antibody may also be used in  
CC therapy and diagnosis

XX

SQ Sequence 369 AA;

Query Match 98.6%; Score 1909; DB 2; Length 369;

Best Local Similarity 98.6%; Pred. No. 1.4e-186;

Matches 364; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60  
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  

Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120  
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  

Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
       |||: ||||| ||||| :| ||||| ||||| ||||| ||||| |||||  

Db 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KIWGRQIPGTTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  

Db 241 KIWGRQIPGTTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
       ||||| ||||| ||||| ||||| ||||| ||||| |||||  

Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGLPWSLL 369  
       |||||  

Db 361 LSGLPWSLL 369

#### RESULT 3

AAW06124

ID AAW06124 standard; protein; 402 AA.

XX

AC AAW06124;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor.

XX

KW Human; neuropeptide receptor; drug screening; receptor-agonist;  
 KW receptor-antagonist; anorectic; antitumour; anticholesterolemic;  
 KW neuroprotective; anticonvulsant; hypotensive; sedative; diagnostic;  
 KW gene therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 47. .72

FT /note= "Transmembrane region-1"

FT Domain 83. .106

FT /note= "Transmembrane region-2"

FT Domain 112. .142

FT /note= "Transmembrane region-3"

FT Domain 163. .189

FT /note= "Transmembrane region-4"

FT Domain 214. .239  
FT /note= "Transmembrane region-5"  
FT Domain 299. .327  
FT /note= "Transmembrane region-6"  
FT Domain 335. .363  
FT /note= "Transmembrane region-7"  
XX  
PN WO9634877-A1.  
XX  
PD 07-NOV-1996.  
XX  
PF 05-MAY-1995; 95WO-US005616.  
XX  
PR 05-MAY-1995; 95WO-US005616.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Soppet DR, Li Y, Rosen CA;  
XX  
DR WPI; 1996-506094/50.  
DR N-PSDB; AAT42826.  
XX  
PT Human neuro-peptide receptor polypeptide(s) - used to identify  
PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of  
PT obesity, Alzheimer's disease, epilepsy, etc.  
XX  
PS Claim 1; Page 49-50; 77pp; English.  
XX  
CC The sequence represents a human adult hypothalamus neuropeptide receptor,  
CC structurally related to the G-protein-coupled receptor family. Splice  
CC variants are given in AAW06125-26. The receptor contains 7 transmembrane  
CC regions. The receptor may be produced in recombinant form and used in a  
CC drug screening assay for isolation of receptor-agonists and -antagonists,  
CC which may be used as anorectic, antitumour, anticholesterolemic,  
CC neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The  
CC encoding DNA may be used in genetic disease diagnosis or gene therapy.  
CC The receptor itself and its corresponding antibody may also be used in  
CC therapy and diagnosis  
XX  
SQ Sequence 402 AA;  
  
Query Match 97.3%; Score 1884; DB 2; Length 402;  
Best Local Similarity 98.9%; Pred. No. 5.7e-184;  
Matches 359; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFERYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
  
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120  
  
Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy	181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
	:     :     :     :     :     :     :     :     :     :     :
Db	181 AVMECSSVLPPELANRTRLFSVCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300
	:     :     :     :     :     :     :     :     :     :     :
Db	241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300
Qy	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
	:     :     :     :     :     :     :     :     :     :     :
Db	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

RESULT 4

AAU00440

ID AAU00440 standard; protein; 372 AA.

XX

AC AAU00440;

XX

DT 18-JUN-2001 (first entry)

XX

DE Human neuropeptide receptor splice variant 2.

XX

KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;  
 KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;  
 KW cardiovascular disorder; autoimmune disorder; infectious disorder;  
 KW eating behaviour disorder; narcolepsy; neurological disease;  
 KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;  
 KW protein co-ordinate data.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 47. .72

FT /label= TM1

FT /note= "Transmembrane region 1"

FT Region 83. .106

FT /label= TM2

FT /note= "Transmembrane region 2"

FT Region 112. .142

FT /label= TM3

FT /note= "Transmembrane region 3"

FT Region 163. .189

FT /label= TM4

FT /note= "Transmembrane region 4"

FT Region 214. .239

FT /label= TM5

FT /note= "Transmembrane region 5"

FT Region 299. .327

FT /label= TM6

FT /note= "Transmembrane region 6"

FT Region 335. .363

FT /label= TM7

FT /note= "Transmembrane region 7"  
XX  
PN WO200117532-A1..  
XX  
PD 15-MAR-2001.  
XX  
PF 07-SEP-2000; 2000WO-US024518.  
XX  
PR 10-SEP-1999; 99US-00393696.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Soppet DR, Li Y, Rosen CA;  
XX  
DR WPI; 2001-183276/18.  
DR N-PSDB; AAS00493.  
XX  
PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,  
PT useful for preventing, treating or ameliorating obesity, narcolepsy,  
PT neurological disease and addiction to narcotics, nicotine and alcohol.  
XX  
PS Claim 3; Fig 6; 385pp; English.  
XX  
CC The present sequence represents human neuropeptide receptor splice  
CC variant 2. Two splice variants (AAU00439-AAU00440) and a possible mutant  
CC (AAU00442) of a novel human neuropeptide receptor (AAU00438) are  
CC described. The neuropeptide receptor shows sequence homology to the  
CC neuropeptide Y receptor. Polypeptides and polynucleotides of the  
CC neuropeptide receptor are useful for diagnosing, preventing, or treating  
CC a pathological condition in a subject related to the central nervous and  
CC peripheral nervous systems (CNS and PNS). The polypeptides and  
CC polynucleotides may be used to treat hyperproliferative, cardiovascular,  
CC autoimmune, nervous system or infectious disorders e.g. cancer, heart  
CC disease, rheumatoid arthritis, Alzheimer's disease, HIV infection and  
CC diabetes mellitus. In particular they are useful for preventing, treating  
CC or ameliorating a medical condition in a mammal such as obesity/eating  
CC behaviour disorders, narcolepsy, neurological disease, addiction to  
CC narcotics, nicotine and alcohol, chronic pain, acute pain, migraine  
CC headaches and anxiety disorders. The polynucleotides encoding the  
CC neuropeptide receptor can also be used in gene therapy methods for  
CC treating such diseases  
XX  
SQ Sequence 372 AA;  
  
Query Match 96.8%; Score 1875; DB 4; Length 372;  
Best Local Similarity 98.6%; Pred. No. 4.3e-183;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
  
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120  
  
Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSI LGI AVSLAIMVPQA 180  
Qy 181 AVMQSSSVLP ELANRTRLFSILCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSVLP ELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Qy 361 LSG 363  
Db 361 LSG 363

RESULT 5

AAW80805

ID AAW80805 standard; protein; 389 AA.

XX

AC AAW80805;

XX

DT 29-JAN-1999 (first entry)

XX

DE Amino acid sequence of HFGAN72Y a G-protein coupled receptor.

XX

KW G-protein coupled receptor family; HFGAN72Y; mutation; probe; agonist;  
KW antagonist; activation; inhibition; gene therapy; antibody;  
KW immune response; vaccine; HIV-1; HIV-2; cancer; anorexia; bulimia;  
KW asthma; Parkinson's disease; acute heart failure; hypotension;  
KW hypertension; urinary retention; osteoporosis; angina pectoris;  
KW myocardial infarction; ulcer; allergies; psychotic disorder;  
KW neurological disorder; gene mapping.

XX

OS Homo sapiens.

XX

PN EP875565-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308554.

XX

PR 30-APR-1997; 97US-00846705.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis C;

XX

DR WPI; 1998-570286/49.

DR N-PSDB; AAV68511.

XX

PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -  
PT useful as diagnostic reagents and for prevention and treatment of HIV

PT infections, cancer, osteoporosis and Parkinson's disease.

XX  
PS Claim 1; Page 7; 22pp; English.  
XX

CC This is the amino acid sequence of the G-protein coupled receptor,  
CC HFGAN72Y used in the method of the invention. HFGAN72Y polypeptides and  
CC polynucleotides are useful for diagnosing susceptibility to diseases by  
CC detecting mutations in the HFGAN72Y gene using probes containing the  
CC HFGAN72Y nucleotide sequence, and can diagnose diseases associated with  
CC HFGAN72Y imbalance by determining HFGAN72Y polypeptide or mRNA expression  
CC levels. Agonists/antagonists can be used in treatment to activate/inhibit  
CC HFGAN72Y activity, in addition to direct administration of antisense  
CC sequences to prevent expression, or HFGAN72Y polypeptides to treat  
CC conditions associated with a lack HFGAN72Y protein. Gene therapy may also  
CC be used to affect endogenous HFGAN72Y polypeptide production. HFGAN72Y  
CC antibodies are useful for inducing an immune response to immunise and  
CC prevent diseases, and for isolating HFGAN72Y clones or purifying the  
CC polypeptides by affinity chromatography. HFGAN72Y polypeptides can be  
CC administered directly or as a vaccine to inoculate against diseases.  
CC Diseases diagnosed, prevented or treated include HIV-1 or HIV-2  
CC infections, pain, cancers, anorexia, bulimia, asthma, Parkinson's  
CC disease, acute heart failure, hypotension, hypertension, urinary  
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcers;  
CC allergies, benign prostatic hypertrophy, and psychotic and neurological  
CC disorders. The HFGAN72Y polypeptide is also useful for mapping the gene  
CC to a chromosome, allowing gene inheritance to be studied through linkage  
CC analysis

XX  
SQ Sequence 389 AA;

Query Match 96.8%; Score 1875; DB 2; Length 389;  
Best Local Similarity 98.6%; Pred. No. 4.5e-183;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MEPSATPGAQMGVPPGSREPPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLCPASLLVDITESWLFGHALCK 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLCPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
|||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSAVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 KLWGRQIPGTTSAVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363  
|||  
Db 361 LSG 363

RESULT 6

AAU11187

ID AAU11187 standard; protein; 389 AA.

XX

AC AAU11187;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72Y.

XX

KW Human; G protein-coupled receptor; GPCR; HFGAN72Y; bacterial infection;  
KW fungal infection; protozoan infection; viral infection;  
KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;  
KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;  
KW angina pectoris; renal disease; depression; schizophrenia; anorexia;  
KW obesity; Kallman's syndrome; hypothalamic disorder;  
KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;  
KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.

XX

OS Homo sapiens.

XX

PN US2001025031-A1.

XX

PD 27-SEP-2001.

XX

PF 06-APR-2001; 2001US-00828538.

XX

PR 08-JUN-1998; 98US-0088524P.

PR 22-JUL-1998; 98US-0093726P.

PR 08-JUN-1999; 99US-00328014.

XX

PA (ELLI/) ELLIS C E.

PA (KWOK/) KWOK C.

PA (BODS/) BODSWORTH N J.

PA (HALS/) HALSEY W.

PA (HORN/) HORN S V.

XX

PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;

XX

DR WPI; 2001-624968/72.

XX

PT Isolated HFGAN72 receptor useful for treatment of a patient having need  
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.  
PT infections such as bacterial, fungal, protozoan and viral infections and  
PT cancers.

XX

PS Claim 8; Fig 3; 75pp; English.

XX

CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or  
CC its variant, encoded by the 8 exon sequences given in the specification.  
CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the

CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is  
CC administered by providing to the patient DNA encoding HFGAN72 and  
CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly  
CC useful for applications in the detection and treatment of disease, e.g.  
CC infections such as bacterial, fungal, protozoan and viral infections,  
CC particularly infections caused by human immunodeficiency virus (HIV)-1 or  
CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial  
CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,  
CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,  
CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),  
CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,  
CC Huntington's disease and many other diseases and disorders given in the  
CC specification. The present sequence is the human HFGAN72Y receptor being  
CC the product of a splice variant of HFGAN72

XX

SQ Sequence 389 AA;

Query Match 96.8%; Score 1875; DB 4; Length 389;  
Best Local Similarity 98.6%; Pred. No. 4.5e-183;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMVGPPGSREPPSPVPPDYEDEFLRLYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQMVGPPGSREPPSPVPPDYEDEFLRLYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAASLLVDITESWLFHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAASLLVDITESWLFHALCK 120
Qy	121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Qy	181 AVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db	181 AVMECSSSVLPLEANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy	301 MVVLLVFALCYLPISVLNVLRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVLNVLRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

RESULT 7

ABB08208

ID ABB08208 standard; protein; 389 AA.

XX

AC ABB08208;

XX

DT 12-MAR-2002 (first entry)

XX  
DE G-protein coupled receptor (HFGAN72Y).  
XX  
KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;  
KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;  
KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;  
KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder;  
KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium;  
KW schizophrenia; manic depression; dementia; mental retardation;  
KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2.  
XX  
OS Homo sapiens.  
XX  
PN EP1156110-A2.  
XX  
PD 21-NOV-2001.  
XX  
PF 27-OCT-1997; 2001EP-00203010.  
XX  
PR 30-APR-1997; 97US-00846705.  
PR 27-OCT-1997; 97EP-00308554.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Bergsma DJ, Ellis CE;  
XX  
DR WPI; 2002-084320/12.  
DR N-PSDB; ABA96019.  
XX  
PT New polynucleotide encoding a G-protein coupled receptor designated  
PT HFGAN72Y is useful to diagnose and treat associated diseases including  
PT cancer, infection, cardiac disease and psychotic and neurological  
PT disorders.  
XX  
PS Claim 10; Page 7; 22pp; English.  
XX  
CC The sequence represents G-protein coupled receptor HFGAN72Y. The  
CC invention relates to a novel isolated polynucleotide encoding HFGAN72Y  
CC polypeptide. The polypeptide of the invention has cytostatic, cardiant,  
CC analgesic, tranquillising, nootropic, neuroprotective, and anti-asthmatic  
CC activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y  
CC polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a  
CC subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y  
CC antagonist or competitor, or nucleic acid which inhibits HFGAN72Y  
CC expression is used to treat a subject in need of decreased HFGAN72Y  
CC activity or expression. HFGAN72Y-associated diseases include infections,  
CC particularly by HIV-1 or HIV-2, cancers, anorexia, bulimia, Parkinson's  
CC disease, cardiac diseases, ulcers, urinary retention, asthma, allergies,  
CC benign prostatic hypertrophy, and psychotic and neurological disorders  
CC including anxiety, schizophrenia, manic depression, delirium, dementia,  
CC severe mental retardation and dyskinesias such as Huntington's disease  
CC and Tourette's syndrome, and pain  
XX  
SQ Sequence 389 AA;

Query Match 96.8%; Score 1875; DB 5; Length 389;  
Best Local Similarity 98.6%; Pred. No. 4.5e-183;

Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVA 60  
 |||||||  
 Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVA 60  
 |||||||  
 Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120  
 |||||||  
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120  
 |||||||  
 Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
 |||||||  
 Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
 |||||||  
 Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
 ||||:  
 Db 181 AVMECSSVLPLEANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
 ||||:  
 Qy 241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
 |||||||  
 Db 241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
 |||||||  
 Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
 |||||||  
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
 |||||||  
 Qy 361 LSG 363  
 |||  
 Db 361 LSG 363

#### RESULT 8

AAW80456

ID AAW80456 standard; protein; 425 AA.

XX

AC AAW80456;

XX

DT 26-JAN-1999 (first entry)

XX

DE G-protein coupled receptor (HFGAN72X) polypeptide.

XX

KW G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;

KW bulimia; asthma; Parkinson's disease; acute heart failure;

KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;

KW benign prostatic hypertrophy; neurological disorder.

XX

OS Homo sapiens.

XX

PN EP875566-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308563.

XX

PR 30-APR-1997; 97US-00846704.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX  
PI Bergsma DJ, Ellis CE;  
XX  
DR WPI; 1998-559432/48.  
DR N-PSDB; AAV63468.  
XX  
PT New human G-protein coupled receptor HFGAN72X polypeptide and  
PT polynucleotide - useful as diagnostic reagents and for treating e.g. HIV  
PT infection, cancer and Parkinson's disease.  
XX  
PS Claim 1; Page 7-8; 24pp; English.  
XX  
CC The present sequence represents a G-protein coupled receptor (HFGAN72X)  
CC polypeptide. HFGAN72X polypeptides and polynucleotides are useful for  
CC diagnosing diseases related to over or under expression of HFGAN72X  
CC proteins by identifying mutations in the HFGAN72X gene using HFGAN72X  
CC probes, or determining HFGAN72X protein or mRNA expression levels.  
CC HFGAN72X polypeptides are also useful for screening for compounds which  
CC affect activity of the protein. Diseases that can be treated with  
CC HFGAN72X include HIV infections, pain, anorexia, cancers, bulimia,  
CC asthma, Parkinson's disease, acute heart failure, hypotension,  
CC hypertension, urinary retention, osteoporosis, angina pectoris,  
CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy,  
CC and psychotic and neurological disorders  
XX  
SQ Sequence 425 AA;  
  
Query Match 96.8%; Score 1875; DB 2; Length 425;  
Best Local Similarity 98.6%; Pred. No. 5.1e-183;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
Db |||||||  
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLCPASLLVDITESWLFHALCK 120  
Db |||||||  
Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSIILGIWAVSLAIMVPQA 180  
Db |||||||  
Qy 181 AVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db |||:  
Qy 241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db |||||||  
Qy 301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360  
Db |||||||  
Qy 361 LSG 363  
|||

RESULT 9  
AAU11188  
ID AAU11188 standard; protein; 425 AA.  
XX  
AC AAU11188;  
XX  
DT 25-FEB-2002 (first entry)  
XX  
DE Human G protein-coupled receptor HFGAN72X variant.  
XX  
KW Human; G protein-coupled receptor; GPCR; HFGAN72X; bacterial infection;  
KW fungal infection; protozoan infection; viral infection;  
KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;  
KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;  
KW angina pectoris; renal disease; depression; schizophrenia; anorexia;  
KW obesity; Kallman's syndrome; hypothalamic disorder;  
KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;  
KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2001025031-A1.  
XX  
PD 27-SEP-2001.  
XX  
PF 06-APR-2001; 2001US-00828538.  
XX  
PR 08-JUN-1998; 98US-0088524P.  
PR 22-JUL-1998; 98US-0093726P.  
PR 08-JUN-1999; 99US-00328014.  
XX  
PA (ELLI/) ELLIS C E.  
PA (KWOK/) KWOK C.  
PA (BODS/) BODSWORTH N J.  
PA (HALS/) HALSEY W.  
PA (HORN/) HORN S V.  
XX  
PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;  
XX  
DR WPI; 2001-624968/72.  
DR N-PSDB; AAS17464.  
XX  
PT Isolated HFGAN72 receptor useful for treatment of a patient having need  
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.  
PT infections such as bacterial, fungal, protozoan and viral infections and  
PT cancers.  
XX  
PS Claim 23; Fig 6; 75pp; English.  
XX  
CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or  
CC its variant, encoded by the 8 exon sequences given in the specification.  
CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the  
CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is  
CC administered by providing to the patient DNA encoding HFGAN72 and

CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly useful for applications in the detection and treatment of disease, e.g. infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by human immunodeficiency virus (HIV)-1 or HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial infarction, ulcers, asthma, allergies, angina pectoris, renal disease, depression, schizophrenia, anorexia, obesity, Kallman's syndrome, hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism), migraine, pain, lung diseases, burns, sleep disorders, jet lag, Huntington's disease and many other diseases and disorders given in the specification. The present sequence is the human HFGAN72X variant, encoded by an alternative allele of HFGAN72

XX

SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 4; Length 425;  
Best Local Similarity 98.6%; Pred. No. 5.1e-183;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
|||: ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 181 AVMECSSSVLPELANRTRLFSLVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 241 KLWGRQIPGTTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363  
|||

Db 361 LSG 363

RESULT 10

AAU11186

ID AAU11186 standard; protein; 425 AA.

XX

AC AAU11186;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72X.

XX  
KW Human; G protein-coupled receptor; GPCR; HFGAN72X; bacterial infection;  
KW fungal infection; protozoan infection; viral infection;  
KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;  
KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;  
KW angina pectoris; renal disease; depression; schizophrenia; anorexia;  
KW obesity; Kallman's syndrome; hypothalamic disorder;  
KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;  
KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2001025031-A1.  
XX  
PD 27-SEP-2001.  
XX  
PF 06-APR-2001; 2001US-00828538.  
XX  
PR 08-JUN-1998; 98US-0088524P.  
PR 22-JUL-1998; 98US-0093726P.  
PR 08-JUN-1999; 99US-00328014.  
XX  
PA (ELLI/) ELLIS C E.  
PA (KWOK/) KWOK C.  
PA (BODS/) BODSWORTH N J.  
PA (HALS/) HALSEY W.  
PA (HORN/) HORN S V.  
XX  
PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;  
XX  
DR WPI; 2001-624968/72.  
XX  
PT Isolated HFGAN72 receptor useful for treatment of a patient having need  
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.  
PT infections such as bacterial, fungal, protozoan and viral infections and  
PT cancers.  
XX  
PS Claim 8; Fig 2; 75pp; English.  
XX  
CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or  
CC its variant, encoded by the 8 exon sequences given in the specification.  
CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the  
CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is  
CC administered by providing to the patient DNA encoding HFGAN72 and  
CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly  
CC useful for applications in the detection and treatment of disease, e.g.  
CC infections such as bacterial, fungal, protozoan and viral infections,  
CC particularly infections caused by human immunodeficiency virus (HIV)-1 or  
CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial  
CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,  
CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,  
CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),  
CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,  
CC Huntington's disease and many other diseases and disorders given in the  
CC specification. The present sequence is the human HFGAN72X receptor being  
CC the product of a splice variant of HFGAN72  
XX

SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 4; Length 425;  
Best Local Similarity 98.6%; Pred. No. 5.1e-183;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVA 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAIChPllFKStARRARGSiLGIWAVSLAIMVPQA 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAIChPllFKStARRARGSiLGIWAVSLAIMVPQA 180

Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
|||: ||| ||| ||| |||: | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 181 AVMECSSVLPLEANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360

Qy 361 LSG 363  
|||  
Db 361 LSG 363

RESULT 11

AAB67079

ID AAB67079 standard; protein; 425 AA.

XX

AC AAB67079;

XX

DT 10-APR-2001 (first entry)

XX

DE Human HFGAN72 receptor SEQ ID NO: 13.

XX

KW Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72;

KW truncation mutant; ligand; neurodegenerative disorder; pain;

KW eating disorder; behaviour disorder; mood disorder.

XX

OS Homo sapiens.

XX

PN WO200100787-A2.

XX

PD 04-JAN-2001.

XX

PF 22-JUN-2000; 2000WO-US017251.

XX

PR 25-JUN-1999; 99US-0141156P.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;  
XX  
DR WPI; 2001-071483/08.  
XX  
PT Polynucleotides encoding Lig 72A polypeptides or their variants, which  
PT are useful in the treatment of a disease or disorder associated with  
PT pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,  
PT neuropathic pain and back pain.  
XX  
PS Claim 8; Fig 7; 101pp; English.  
XX  
CC The present invention provides the protein and coding sequences for the  
CC human, mouse and rat HFGAN receptor ligand Lig72A. It also provides  
CC truncated mutant versions. These, and their agonists and antagonists, are  
CC all useful in the treatment of eating, neurodegenerative, behaviour,  
CC mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy  
CC and acute inflammatory conditions  
XX  
SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 4; Length 425;  
Best Local Similarity 98.6%; Pred. No. 5.1e-183;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
Db |||||||  
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120  
Db |||||||  
Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
Db |||||||  
Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db ||||:  
Qy 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db |||||||  
Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
Db |||||||  
Qy 361 LSG 363  
Db |||  
Qy 361 LSG 363

RESULT 12

AAG78345

ID AAG78345 standard; protein; 425 AA.

XX

AC AAG78345;

XX

DT 22-JAN-2002 (first entry)

XX

DE Human HFGAN72X G coupled receptor polypeptide.

XX

KW Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;  
KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;  
KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;  
KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;  
KW Parkinson's disease; acute heart failure; hypotension; hypertension;  
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;  
KW ulcers; asthma; allergy; delirium; dementia;  
KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;  
KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor.

XX

OS Homo sapiens.

XX

PN EP1154019-A2.

XX

PD 14-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203008.

XX

PR 30-APR-1997; 97US-00846704.

PR 27-OCT-1997; 97EP-00308563.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-012659/02.

DR N-PSDB; AAI64172.

XX

PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and  
PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's  
PT disease, and acute heart failure.

XX

PS Claim 11; Page 7-8; 24pp; English.

XX

CC The present sequence is that of a human HFGAN72X polypeptide encoded by a  
CC cDNA shown in AAI64172. The specification describes a newly isolated  
CC polynucleotide encoding a HFGAN72X G coupled receptor polypeptide. The  
CC protein of the invention has antibacterial, fungicide, virucide,  
CC protozoacide, anti-HIV, cardiant, analgesic, cytostatic, nootropic,  
CC antiparkinsonian, antiulcer, antiasthmatic, tranquiliser, neuroleptic,  
CC antidepressant, anticonvulsant and osteopathic activities. HFGAN72X  
CC polynucleotides (PNs) are used to express HFGAN72X in vivo, to treat  
CC diseases requiring increased activity or expression of HFGAN72X; for  
CC recombinant production of HFGAN72X; diagnose diseases by detecting  
CC mutations in genomic sequences and in chromosome identification and  
CC mapping. HFGAN72X polypeptides are used to raise specific antibodies; as

CC therapeutic agents; to identify HFGAN72X protein-expressing clones; to  
CC purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X  
CC PNs are used to identify (ant)agonists of HFGAN72X, useful  
CC therapeutically. Nucleic acids that inhibit expression of HFGAN72X and  
CC polypeptides that compete with ligands for binding to HFGAN72X proteins  
CC are also useful therapeutically and diagnostically. HFGAN72X-related  
CC diseases include infections (bacterial, viral, fungal or protozoal,  
CC particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's  
CC disease; acute heart failure; hypotension; hypertension; urinary  
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;  
CC asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;  
CC manic depression; delirium; dementia; severe mental retardation and  
CC dyskinesias

XX

SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 5; Length 425;  
Best Local Similarity 98.6%; Pred. No. 5.1e-183;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120
Qy	121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180
Qy	181 AVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db	181 AVMECSSVLPLEANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

RESULT 13

ABP81941

ID ABP81941 standard; protein; 425 AA.

XX

AC ABP81941;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human orexin receptor 1 protein SEQ ID NO:368.  
XX  
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer.  
XX  
OS Homo sapiens.  
XX  
PN WO200261087-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 19-DEC-2001; 2001WO-US050107.  
XX  
PR 19-DEC-2000; 2000US-0257144P.  
XX  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
PI Burmer GC, Roush CL, Brown JP;  
XX  
DR WPI; 2003-046718/04.  
DR N-PSDB; ABZ42789.  
XX  
PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.  
XX  
PS Disclosure; Fig 1; 523pp; English.  
XX  
CC The present invention describes antigenic peptides (I) comprising: (a)  
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related disease, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory

CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention

XX

SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 6; Length 425;  
Best Local Similarity 98.6%; Pred. No. 5.1e-183;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSVLPLEANRTRLFSILCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300.

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363  
Db 361 LSG 363

RESULT 14

ABG75058

ID ABG75058 standard; protein; 425 AA.

XX

AC ABG75058;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human orexin receptor 1 protein.

XX

KW Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;  
KW gene therapy; anorectic; immunomodulator; antidiabetic; hypotensive;  
KW cardiant; osteopathic; antilipemic.

XX

OS Homo sapiens.

XX  
PN WO2003075945-A2.  
XX  
PD 18-SEP-2003.  
XX  
PF 14-MAR-2003; 2003WO-EP002714.  
XX  
PR 14-MAR-2002; 2002EP-00005882.  
PR 15-MAR-2002; 2002EP-00006012.  
PR 20-MAR-2002; 2002EP-00006271.  
PR 25-MAR-2002; 2002EP-00006810.  
XX  
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
XX  
PI Eulenberg K, Steuernagel A, Haeder T, Broenner G;  
XX  
DR WPI; 2003-748334/70.  
DR N-PSDB; ACH00818.  
XX  
PT New pharmaceutical composition comprising a nucleic acid molecule  
PT encoding proteins regulating the energy homeostasis and metabolism of  
PT triglycerides useful for detecting or preventing metabolic diseases, e.g.  
PT obesity.  
XX  
PS Claim 3; Fig 7G; 140pp; English.  
XX  
CC The present invention relates to pharmaceutical compositions comprising  
CC the coding sequences shown in ACH00815-ACH00827, or their encoded  
CC proteins (shown in ABG75054, ABG75056-ABG75067). These are proteins  
CC involved in the metabolism of triglycerides and in energy homeostasis,  
CC and their coding sequences. The composition is useful for the manufacture  
CC of an agent for detecting, verifying, treating, alleviating or preventing  
CC disorders, including metabolic diseases such as obesity and other body-  
CC weight regulation disorders as well as related disorders such as  
CC metabolic syndrome, eating disorder, cachexia, diabetes mellitus,  
CC hypertension, coronary heart disease, hypercholesterolaemia,  
CC dyslipidaemia, osteoarthritis or gallstones, in cells, cell masses,  
CC organs or subjects. The coding sequences can be used in the production of  
CC transgenic animals which under- or over-produce the gene of interest. The  
CC present sequence is a protein of the invention  
XX  
SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 7; Length 425;  
Best Local Similarity 98.6%; Pred. No. 5.1e-183;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLYIWRDYLKPQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLYIWRDYLKPQYEWVLIAAYVAVFVVA 60  
  
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120  
  
Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Db 121 VIPYLQAVSVSVALTLSFIALDRWYATICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180  
Qy 181 AVMQSSVLP E LANRTRLFSL CHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
|||: |||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Db 181 AVMECSSVLP E LANRTRLF SVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLS GEPQPRGRAFLAEVKQMRARRKAKML 300  
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLS GEPQPRGRAFLAEVKQMRARRKAKML 300  
Qy 301 MVVLLVFALCYLP ISV LNV LKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Db 301 MVVLLVFALCYLP ISV LNV LKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
Qy 361 LSG 363  
|||:  
Db 361 LSG 363

## RESULT 15

ADK52564

ID ADK52564 standard; protein; 425 AA.

XX

AC ADK52564;

XX

DT 06-MAY-2004 (first entry)

XX

DE Hematological disorder associated Gene ID 14393 encoded protein.

XX

KW cytostatic; antianemic; antisickling; virucide; hemostatic; nephrotropic;  
KW cytostatic; thrombolytic; antiparasitic; gene therapy;  
KW hematologic disorder; cancer; Sickle Cell Anemia;  
KW Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;  
KW Retinoblastoma; Hemophilia; Thrombosis; Herpes; Thalassemia;  
KW transfusion reaction; Erythroblastosis; mechanical trauma;  
KW micro-angiopathic hemolytic anemia; parasite infection.

XX

OS Homo sapiens.

XX

PN WO2003065871-A2.

XX

PD 14-AUG-2003.

XX

PF 28-JAN-2003; 2003WO-US002484.

XX

PR 04-FEB-2002; 2002US-0354333P.  
PR 28-FEB-2002; 2002US-0360258P.  
PR 15-MAR-2002; 2002US-0364476P.  
PR 26-APR-2002; 2002US-0375626P.  
PR 06-JUN-2002; 2002US-0386494P.  
PR 24-JUN-2002; 2002US-0390965P.  
PR 28-JUN-2002; 2002US-0392480P.  
PR 03-JUL-2002; 2002US-0394128P.  
PR 31-JUL-2002; 2002US-0399783P.  
PR 13-AUG-2002; 2002US-0403221P.  
PR 30-AUG-2002; 2002US-0407045P.  
PR 25-NOV-2002; 2002US-0429048P.

XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Carroll JM, Healy A, Weich NS, Kelly LM;  
XX  
DR WPI; 2003-731464/69.  
DR N-PSDB; ADK52563.  
XX  
PT Identifying a compound capable of treating a hematologic disorder (e.g. anemia or leukemia) comprises assaying the ability of the compound to modulate the expression or activity of e.g. 131,148, 199 or 12303 polypeptide or nucleic acid.  
XX  
PS Disclosure; SEQ ID NO 22; 232pp; English.  
XX  
CC The invention relates to a method of identifying a compound capable of treating a hematologic disorder comprises assaying the ability of the compound to modulate 131,148, 199, 12303, 13906, 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 or 13249 nucleic acid expression or polypeptide activity, thus, identifying a compound capable of treating a hematologic disorder. The methods are useful in diagnosing, preventing and treating hematological disorders, such as cancer, Sickle Cell Anemia, Infectious Mononucleosis, Leukemia, Polycythemia Vera, Lymphoma, Retinoblastoma, Hemophilia, disorders associated with an increased risk of Thrombosis, Herpes, Thalassemia, antibody-mediated disorders such as transfusion reactions and Erythroblastosis, mechanical trauma to red blood cells such as microangiopathic hemolytic anemias, infections by parasites or chemical injuries. The methods may also be used for identifying compounds that modulate hematological disorders. This sequence corresponds to the protein encoded by one of the genes modulated by the compounds.  
XX  
SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 7; Length 425;  
Best Local Similarity 98.6%; Pred. No. 5.1e-183;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLEVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSVLPLEANRTRLFLSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
|||: ||| ||| ||| ||| :| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRTAKML 300  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300  
Qy 301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360  
Qy 361 LSG 363  
Db 361 LSG 363

Search completed: October 14, 2004, 10:50:38  
Job time : 90.9271 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2004, 10:43:25 ; Search time 22.4691 Seconds  
(without alignments)  
1089.110 Million cell updates/sec

Title: US-10-070-532-4

Perfect score: 1937

Sequence: 1 MEPSATPGAQMGVPPGSREP.....NSAANPIIYNFLSGLPWSLL 369

Scoring table: BLOSUM62

Gapext 0.5 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	1909	98.6	369	4	US-08-462-509B-4	Sequence 4, Appli
2	1909	98.6	369	5	PCT-US95-05616-4	Sequence 4, Appli
3	1875	96.8	377	5	PCT-US95-05616-6	Sequence 6, Appli
4	1875	96.8	389	2	US-08-846-705-2	Sequence 2, Appli
5	1875	96.8	389	4	US-09-211-823C-23	Sequence 23, Appli
6	1875	96.8	402	4	US-08-462-509B-2	Sequence 2, Appli
7	1875	96.8	402	5	PCT-US95-05616-2	Sequence 2, Appli
8	1875	96.8	425	3	US-08-846-704-2	Sequence 2, Appli
9	1875	96.8	425	4	US-09-211-823C-22	Sequence 22, Appli
10	1872	96.6	372	4	US-08-462-509B-6	Sequence 6, Appli
11	1869	96.5	402	3	US-08-846-704-4	Sequence 4, Appli

12	1869	96.5	425	3	US-09-479-128-2	Sequence 2, Appli
13	1313.5	67.8	444	4	US-09-426-290-2	Sequence 2, Appli
14	1312.5	67.8	444	3	US-09-119-788-2	Sequence 2, Appli
15	1279	66.0	263	3	US-08-513-974B-54	Sequence 54, Appli
16	1279	66.0	263	3	US-08-513-974B-376	Sequence 376, App
17	1279	66.0	263	4	US-09-461-436B-54	Sequence 54, Appli
18	483.5	25.0	430	3	US-09-255-368-8	Sequence 8, Appli
19	483.5	25.0	430	4	US-09-405-558-8	Sequence 8, Appli
20	480.5	24.8	432	3	US-09-255-368-2	Sequence 2, Appli
21	480.5	24.8	432	4	US-09-405-558-2	Sequence 2, Appli
22	473.5	24.4	420	3	US-09-255-368-6	Sequence 6, Appli
23	473.5	24.4	420	4	US-09-405-558-6	Sequence 6, Appli
24	467.5	24.1	417	4	US-09-405-558-44	Sequence 44, Appli
25	415	21.4	370	3	US-09-172-353-2	Sequence 2, Appli
26	415	21.4	370	3	US-09-172-353-3	Sequence 3, Appli
27	415	21.4	370	4	US-09-799-955-2	Sequence 2, Appli
28	415	21.4	370	4	US-09-799-955-3	Sequence 3, Appli
29	411.5	21.2	370	3	US-09-172-353-7	Sequence 7, Appli
30	411.5	21.2	370	4	US-09-799-955-7	Sequence 7, Appli
31	411	21.2	370	3	US-08-513-974B-26	Sequence 26, Appli
32	411	21.2	370	3	US-08-513-974B-323	Sequence 323, App
33	411	21.2	370	3	US-09-172-353-5	Sequence 5, Appli
34	411	21.2	370	3	US-08-776-971-21	Sequence 21, Appli
35	411	21.2	370	3	US-08-776-971-104	Sequence 104, App
36	411	21.2	370	4	US-09-799-955-5	Sequence 5, Appli
37	411	21.2	370	4	US-09-461-436B-26	Sequence 26, Appli
38	411	21.2	370	4	US-09-576-290-21	Sequence 21, Appli
39	411	21.2	370	4	US-09-576-290-104	Sequence 104, App
40	404.5	20.9	370	3	US-08-776-971-140	Sequence 140, App
41	404.5	20.9	370	4	US-09-576-290-140	Sequence 140, App
42	401.5	20.7	369	4	US-09-170-496D-178	Sequence 178, App
43	400.5	20.7	369	3	US-09-172-353-6	Sequence 6, Appli
44	400.5	20.7	369	4	US-09-799-955-6	Sequence 6, Appli
45	400.5	20.7	369	4	US-09-170-496D-26	Sequence 26, Appli

#### ALIGNMENTS

#### RESULT 1

US-08-462-509B-4

```
; Sequence 4, Application US/08462509B
; Patent No. 6410701
; GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor and
;   NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: MD
;   COUNTRY: USA
;   ZIP: 20850
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
```

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,509B  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US95/05616  
; FILING DATE: 05-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wales, Michele M.  
; REGISTRATION NUMBER: 43,975  
; REFERENCE/DOCKET NUMBER: PF168P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 369 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-462-509B-4

Query Match 98.6%; Score 1909; DB 4; Length 369;  
Best Local Similarity 98.6%; Pred. No. 2.6e-188;  
Matches 364; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGVPPGSREPPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMVGVPPGSREPPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFR 240  
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFR 240

Qy 241 KLGGRQIPGTTSLVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLGGRQIPGTTSLVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGLPWSLL 369  
Db 361 LSGLPWSLL 369

RESULT 2

PCT-US95-05616-4

; Sequence 4, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/05616

; FILING DATE: concurrently

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-268

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 369 BASE PAIRS

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE: cDNA

PCT-US95-05616-4

Query Match 98.6%; Score 1909; DB 5; Length 369;

Best Local Similarity 98.6%; Pred. No. 2.6e-188;

Matches 364; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MEPSATPGAMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Db : |||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Db 181 AVMECSSVLPPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
  
Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300  
Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300  
  
Qy 301 MVVLLVFALCYLPISVNLKR VFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVNLKR VFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
  
Qy 361 LSGLPWSLL 369  
Db 361 LSGLPWSLL 369

## RESULT 3

PCT-US95-05616-6

; Sequence 6, Application PC/TUS9505616  
; GENERAL INFORMATION:  
; APPLICANT: LI, ET AL.  
; TITLE OF INVENTION: Human Neuropeptide Receptor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05616  
; FILING DATE: concurrently  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 377 BASE PAIRS  
; TYPE: AMINO ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: cDNA

PCT-US95-05616-6

Query Match 96.8%; Score 1875; DB 5; Length 377;

Best Local Similarity 98.6%; Pred. No. 8.6e-185;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
Qy	121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180
Qy	181 AVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
	:             :
Db	181 AVMECSSVLPLEANRTRLFSLCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

#### RESULT 4

US-08-846-705-2

; Sequence 2, Application US/08846705

; Patent No. 5935814

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,705

; FILING DATE: 30-APR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-70003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 389 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-846-705-2

Query Match 96.8%; Score 1875; DB 2; Length 389;  
Best Local Similarity 98.6%; Pred. No. 9e-185;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60
Db	1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPAASLLVDITESWLFGHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPAASLLVDITESWLFGHALCK 120
Qy	121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Qy	181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
	:         :
Db	181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLGGRQIPGTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300
Db	241 KLGGRQIPGTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300
Qy	301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

RESULT 5  
US-09-211-823C-23  
; Sequence 23, Application US/09211823C  
; Patent No. 6664229

; GENERAL INFORMATION:  
; APPLICANT: HAGEN, JAMES JOSEPH  
; APPLICANT: TERRETT, JONATHAN ALEXANDER  
; APPLICANT: UPTON, NEIL  
; APPLICANT: PIPER, DAVID  
; APPLICANT: SMITH, MARTIN IAN  
; APPLICANT: KENNEDY, GUY ANTHONY  
; APPLICANT: PATEL, SARASWATI R.  
; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS  
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR  
; TITLE OF INVENTION: ANTAGONISTS THEREOF  
; FILE REFERENCE: P50745  
; CURRENT APPLICATION NUMBER: US/09/211,823C  
; CURRENT FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: US 60/069,459  
; PRIOR FILING DATE: 1997-12-15  
; PRIOR APPLICATION NUMBER: US 60/069,785  
; PRIOR FILING DATE: 1997-12-16  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 389  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-211-823C-23

Query Match 96.8%; Score 1875; DB 4; Length 389;  
Best Local Similarity 98.6%; Pred. No. 9e-185;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSLVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLWGRQIPGTTSLVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360

Qy 361 LSG 363  
Db 361 LSG 363

RESULT 6

US-08-462-509B-2

; Sequence 2, Application US/08462509B  
; Patent No. 6410701  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel et al  
; TITLE OF INVENTION: Human Neuropeptide Receptor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,509B  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US95/05616  
; FILING DATE: 05-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wales, Michele M.  
; REGISTRATION NUMBER: 43,975  
; REFERENCE/DOCKET NUMBER: PF168P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 402 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-462-509B-2

Query Match 96.8%; Score 1875; DB 4; Length 402;  
Best Local Similarity 98.6%; Pred. No. 9.4e-185;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLCPASLLVDITESWLFHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLCPASLLVDITESWLFHALCK 120

Qy 121 VIPYIQLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180

Db           ||||||||||||||||||| 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
Qy           181 AVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
              |||: |||||||||||||:| |||||||||||||||||||||||||||||||||  
Db           181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Qy           241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300  
              |||||||||||||||||||||||||||||||||||||||||||||||  
Db           241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300  
Qy           301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360  
              |||||||||||||||||||||||||||||||||||||||||||  
Db           301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360  
Qy           361 LSG 363  
              |||  
Db           361 LSG 363

RESULT 7

PCT-US95-05616-2

; Sequence 2, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/05616

; FILING DATE: concurrently

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-268

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 402 AMINO ACIDS

; TYPE: AMINO ACID

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN

PCT-US95-05616-2

Query Match 96.8%; Score 1875; DB 5; Length 402;  
Best Local Similarity 98.6%; Pred. No. 9.4e-185;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60  
|||||  
Db 1 MEPSATPGAQMGVPPGSREPPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLCPASLLVDITESWLFGHALCK 120  
|||||  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLCPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
|||||  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
|||:  
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300  
|||||  
Db 241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360  
|||||  
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360

Qy 361 LSG 363  
|||  
Db 361 LSG 363

RESULT 8

US-08-846-704-2

; Sequence 2, Application US/08846704

; Patent No. 6020157

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E.

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/846,704  
; FILING DATE: 30-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-70002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 425 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-846-704-2

Query Match 96.8%; Score 1875; DB 3; Length 425;  
Best Local Similarity 98.6%; Pred. No. 1e-184;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQMGVPPGSREPPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120
Qy	121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Qy	181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db	181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLGWGRQIPGTT SALVRNWKPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KLGWGRQIPGTT SALVRNWKPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy	301 MVVLLVFALCYLPISVNLKRVFGMFHQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVNLKRVFGMFHQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

RESULT 9  
US-09-211-823C-22  
; Sequence 22, Application US/09211823C  
; Patent No. 6664229  
; GENERAL INFORMATION:  
; APPLICANT: HAGEN, JAMES JOSEPH  
; APPLICANT: TERRETT, JONATHAN ALEXANDER  
; APPLICANT: UPTON, NEIL  
; APPLICANT: PIPER, DAVID  
; APPLICANT: SMITH, MARTIN IAN  
; APPLICANT: KENNEDY, GUY ANTHONY  
; APPLICANT: PATEL, SARASWATI R.  
; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS  
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR  
; TITLE OF INVENTION: ANTAGONISTS THEREOF  
; FILE REFERENCE: P50745  
; CURRENT APPLICATION NUMBER: US/09/211,823C  
; CURRENT FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: US 60/069,459  
; PRIOR FILING DATE: 1997-12-15  
; PRIOR APPLICATION NUMBER: US 60/069,785  
; PRIOR FILING DATE: 1997-12-16  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-211-823C-22

Query Match 96.8%; Score 1875; DB 4; Length 425;  
Best Local Similarity 98.6%; Pred. No. 1e-184;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSVLPLEANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363  
|||  
Db 361 LSG 363

## RESULT 10

US-08-462-509B-6

; Sequence 6, Application US/08462509B  
; Patent No. 6410701  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel et al  
; TITLE OF INVENTION: Human Neuropeptide Receptor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,509B  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US95/05616  
; FILING DATE: 05-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wales, Michele M.  
; REGISTRATION NUMBER: 43,975  
; REFERENCE/DOCKET NUMBER: PF168P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 372 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-462-509B-6

Query Match 96.6%; Score 1872; DB 4; Length 372;  
Best Local Similarity 98.3%; Pred. No. 1.7e-184;  
Matches 357; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMVGPPGSRDPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFITVNLSDLADLVTACILCPASLLVDITESWLFHALCK 120  
Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Qy 241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Qy 361 LSG 363  
Db 361 LSG 363

RESULT 11

US-08-846-704-4

; Sequence 4, Application US/08846704

; Patent No. 6020157

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E.

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,704

; FILING DATE: 30-APR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 402 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-846-704-4

Query Match 96.5%; Score 1869; DB 3; Length 402;  
Best Local Similarity 98.3%; Pred. No. 3.9e-184;  
Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363  
Db 361 LSG 363

RESULT 12

US-09-479-128-2

; Sequence 2, Application US/09479128  
; Patent No. 6319710  
; GENERAL INFORMATION:  
; APPLICANT: Berglind Ran Olafsdottir  
; APPLICANT: Jeffrey Gulcher  
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE  
; FILE REFERENCE: 2345.1005-001  
; CURRENT APPLICATION NUMBER: US/09/479,128  
; CURRENT FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/379,083

; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-479-128-2

Query Match 96.5%; Score 1869; DB 3; Length 425;  
Best Local Similarity 98.3%; Pred. No. 4.2e-184;  
Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEPSATPGAMGVPPGSREPSPVPPDYEDEFRLYLRDYLKPQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAMGVPPGSREPSPVPPDYEDEFRLYLRDYLKPQYEWVLIAAYVAVFVVA 60  
  
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFHALCK 120  
  
Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
  
Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
  
Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300  
  
Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
  
Qy 361 LSG 363  
Db 361 LSG 363

RESULT 13  
US-09-426-290-2  
; Sequence 2, Application US/09426290  
; Patent No. 6410712  
; GENERAL INFORMATION:  
; APPLICANT: Berglind Ran Olafsdottir  
; APPLICANT: Jeffrey Gulcher  
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE  
; FILE REFERENCE: 2345.2001-000  
; CURRENT APPLICATION NUMBER: US/09/426,290  
; CURRENT FILING DATE: 1999-10-25  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 444

; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-426-290-2

Query Match 67.8%; Score 1313.5; DB 4; Length 444;  
 Best Local Similarity 70.0%; Pred. No. 7.8e-127;  
 Matches 250; Conservative 37; Mismatches 49; Indels 21; Gaps 3;

Qy 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAWRHNH 75  
      ::|||  |  |||:|  |||||||W|||:|||:|||:|  |||||||  |:  |||||||:|||  |||:|||:  
Pb 24 TOEPELNPTDYYDDEFFLRYLWDEFLYIHPKEYEWVLIAGYLIVEVVALLGNVILCVVAVWKNH 83

Qy 76 HMRTVTNYFIVNLSLADLVTAICLPA~~S~~LLVDITESWLFGHALCKV~~I~~PY~~L~~QAVSVSVAL 135  
|||||:|||||:|| :|||||:|| | :|||||:|| |||:|||

Qy 136 TLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAMQSSVLPelanr 195  
||||| ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Qy 196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTT SALV 255

DB 204 TTLFTVCDERWGGETYPKMYHICFFLVTYMAPLCLMVIALYLQ1FRKLWCRQ1PGTSSVVQ 263

Qv 256 BNWKRPDSLQDLEOGLSGEPOPRG-----RAELAEVKOMBARRKTAKMLMVVLLV 306

Db 264 RKWK-----PLQPVSQPRGPQPTKSRMSAVAAEIKQIRARRKTARMLMVLLV 312

Qy 307 FALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNFLSG 363  
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 313 FAICYLPISILNVLKRVFGMFAHTEDRETVYAWFTFSHLVYANSAANPIIYNFLSG 369

RESULT 14

US-09-119-788-2

; Sequence 2, Application US/09119788

; Patent No. 6166193

; GENERAL INFORMATION:

; APPLICANT: Yanagisawa, Masashi

; TITLE OF INVENTION: CDNA CLONE MY1 THAT ENCODES

; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; . . . CITY: King of Pr

; STATE: PA

; COUNTRY: United States of America

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/119,788

; FILING DATE: 21-JUL-1998

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/053,790  
; FILING DATE: 25-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: King, William T  
; REGISTRATION NUMBER: 30,954  
; REFERENCE/DOCKET NUMBER: GH50029  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5515  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 444 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-09-119-788-2

Query Match 67.8%; Score 1312.5; DB 3; Length 444;  
Best Local Similarity 70.0%; Pred. No. 9.9e-127;  
Matches 250; Conservative 37; Mismatches 49; Indels 21; Gaps 3;

Qy 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75  
::|| | ||:| |||||||:||:||:|||||:|| ||||||:|| ||:||:||:||  
Db 24 TQEPEFLNPTDYZDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAVL 135  
||||| ||||| ||||| ||||| ||||:||:|||||:|| || :||||| ||| |||||:||  
Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSL 143

Qy 136 TLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQAAVMQSSSVLPELANR 195  
||| | ||||| ||||:||||:||| ||: ||| || ||:||| ||: ||| | |||:  
Db 144 TLSCLIALDRWYAICHPLMFKSTAKRARNNSIVIIVSCIIIMIPQAIIVMECSTVFPGLANK 203

Qy 196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSLV 255  
| ||:|| ||| :|||:||| |||:|||:||| || :|| ||||||| |||||:|| :  
Db 204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVAYLQIFRKLWCRQIPGTSSVQ 263

Qy 256 RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306  
| || | ||| | ||| | ||| | ||:||:||| |||:||| |||  
Db 264 RKWK-----PLQPVSQPRPGPGQPTKSRMGAVAEEIKQIRARRKTARMLMVLLV 312

Qy 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 353  
||:|||||:||||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 313 FAICYLPISILNVLKRVFGMFAHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 15  
US-08-513-974B-54  
; Sequence 54, Application US/08513974B  
; Patent No. 6114139  
; GENERAL INFORMATION:  
; APPLICANT: Hinuma, Shuji  
; APPLICANT: Hosoya, Masaki

; APPLICANT: Fujii, Ryo  
; APPLICANT: Ohtaki, Tetsuya  
; APPLICANT: Fukusumi, Shoji  
; APPLICANT: Ohgi, Kazuhiro  
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
; NUMBER OF SEQUENCES: 380  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/513,974B  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP95/01599  
; FILING DATE: 10-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-093989  
; FILING DATE: 19-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-057186  
; FILING DATE: 16-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-007177  
; FILING DATE: 20-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-326611  
; FILING DATE: 28-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-270017  
; FILING DATE: 02-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-236357  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-236356  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189274  
; FILING DATE: 11-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189273  
; FILING DATE: 11-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189272  
; FILING DATE: 11-AUG-1994  
; ATTORNEY/AGENT INFORMATION:

; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 45753  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 263 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-513-974B-54

Query Match 66.0%; Score 1279; DB 3; Length 263;  
Best Local Similarity 94.3%; Pred. No. 1.4e-123;  
Matches 248; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy	91 ADVLVTAICLPPASLLVDITESWLFGHALCKVIPYLQAVSVSVALTLSFIPLD RWYAICH 150
Db	1 ADVLVTAICLPPASLLVDITESWLFGHALCKVIPYLQAVSVVVTLSSIALDRWYAICH 60
Qy	151 PLLFKSTARRARGSILGIWAVSLAIMVPQAAVMQSSSVLPLEANRTRLFSLCHE WADDL 210
	:       :                   :
Db	61 PLLFKSTARRARGSILGIWAVSLAVMVPQAAVMECSSVLPLEANRTRLLSVC DERWADDL 120
Qy	211 YPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTT SALVRNWKRP SDQLGDLEQ 270
Db	121 YPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTT SALVRNWKRP SDQLDDQGQ 180
Qy	271 GLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISV LNVLKRVFGMFRQA 330
Db	181 GLSSEPQPRARAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISV LNVLKRVFGMFRQA 240
Qy	331 SDREAVYACFTFSHWLVYANSAA 353
	:
Db	241 SDREAIYACFTFSHWLVYANSAA 263

Search completed: October 14, 2004, 10:58:12

Job time : 23.4691 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2004, 10:42:40 ; Search time 19.6209 Seconds  
(without alignments)  
1809.496 Million cell updates/sec

Title: US-10-070-532-4

Perfect score: 1937

Sequence: 1 MEPSATPGAQMGVPPGSREP.....NSAANPIIYNFLSGLPWSLL 369

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	422.5	21.8	449	2	A41738	neuropeptide Y rec
2	411.5	21.2	370	1	I52315	G protein-coupled
3	392	20.2	381	2	I39187	neuropeptide Y/pep
4	392	20.2	427	2	S50150	gastric CCK-A rece
5	388	20.0	584	2	JC7809	sulfakinin recepto
6	385.5	19.9	519	2	S17783	tachykinin recepto
7	384.5	19.9	452	2	A34916	neurokinin 3 recep
8	384	19.8	465	1	JQ1517	neurokinin 3 recep
9	378.5	19.5	385	2	S55524	neurokinin 3 recep
10	374.5	19.3	428	2	JN0692	cholecystokinin ty
11	373.5	19.3	452	2	JC2459	gastrin/cholecysto
12	371.5	19.2	450	2	JQ1614	gastrin receptor -
13	371	19.2	349	2	I59336	galanin receptor 1

14	370.5	19.1	430	2	I51898	cholecystokinin A
15	370.5	19.1	440	2	A44081	kappa-type opioid
16	370.5	19.1	452	2	A46195	cholecystokinin B
17	367.5	19.0	402	2	I56595	neurokinin 2 recep
18	367	18.9	447	2	A47430	gastrin/cholecysto
19	365.5	18.9	384	1	S00516	neurokinin 2 recep
20	365.5	18.9	398	1	JQ1059	neurokinin 2 recep
21	364.5	18.8	423	2	B40470	glucocorticoid-ind
22	363.5	18.8	387	2	JC5949	galanin receptor 2
23	362	18.7	366	2	S71152	neuropeptide Y/pep
24	362	18.7	444	2	A42685	cholecystokinin re
25	360	18.6	453	2	S32817	gastrin receptor -
26	359.5	18.6	384	2	I57957	neurokinin 2 recep
27	358.5	18.5	390	2	A36737	neurokinin 2 recep
28	356.5	18.4	407	2	S23510	neurokinin 1 recep
29	354.5	18.3	407	1	JQ1274	neurokinin 1 recep
30	352.5	18.2	480	2	I53053	beta 1 adrenergic
31	352	18.2	423	2	JC7677	allatostatin recep
32	351.5	18.1	407	2	A34357	neurokinin 1 recep
33	351	18.1	394	2	JC7209	galanin receptor -
34	351	18.1	477	1	QRHUB1	beta-1-adrenergic
35	350.5	18.1	407	2	S20304	neurokinin 1 recep
36	349.5	18.0	436	2	JC5599	cholecystokinin-A
37	346.5	17.9	384	2	S20303	neurokinin 2 recep
38	346.5	17.9	443	2	D40470	glucocorticoid-ind
39	346.5	17.9	504	2	A41783	tachykinin recepto
40	345	17.8	390	2	B41007	bombesin receptor,
41	340	17.6	483	2	A25896	beta-adrenergic re
42	338.5	17.5	466	2	S36794	beta-1-adrenergic
43	337	17.4	464	2	S12591	beta-1-adrenergic
44	336	17.3	398	2	JN0708	thyrotropin-releas
45	336	17.3	411	2	I56444	thyrotrophin-relea

## ALIGNMENTS

### RESULT 1

A41738

neuropeptide Y receptor - fruit fly (*Drosophila melanogaster*)

N;Alternate names: G protein-coupled receptor PR4

C;Species: *Drosophila melanogaster*

C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004

C;Accession: A41738

R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.

J. Biol. Chem. 267, 19-12, 1992

A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide Y receptor from *Drosophila melanogaster*.

A;Reference number: A41738; MUID:92112730; PMID:1370455

A;Accession: A41738

A;Molecule type: mRNA

A;Residues: 1-449 <LIA>

A;Cross-references: UNIPROT:P25931; GB:M81490; NID:g157996; PIDN:AAA28727.1;

PID:g157997

C;Genetics:

A;Gene: FlyBase:NepYr

A;Cross-references: FlyBase:FBgn0004842

C;Superfamily: neurokinin 1 receptor  
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 21.8%; Score 422.5; DB 2; Length 449;  
 Best Local Similarity 30.4%; Pred. No. 1e-28;  
 Matches 105; Conservative 59; Mismatches 126; Indels 55; Gaps 9;

## RESULT 2

I52315

## G protein-coupled receptor UHR-1 - rat

C;Species: Rattus sp. (rat)

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 19-May-2000

C;Accession: I52315

R; Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.

Biochem. Biophys. Res. Commun. 209, 606-613, 1995

A;Title: Sequence and tissue distribution of a candidate G-coupled receptor cloned from rat hypothalamus.

A; Reference number: I52315; MUID: 95251659; PMID: 7733930

A;Accession: I52315

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A:Residues: 1-370 <RES>

A;Cross-references: GB:S77867; NID:g998527; PIDN:AAB34129.1; PID:g998528

C:Superfamily: neuropeptid receptor

Query Match 21.2%; Score 411.5; DB 1; Length 370;  
 Best Local Similarity 30.9%; Pred. No. 7.5e-28;  
 Matches 99; Conservative 62; Mismatches 118; Indels 41; Gaps 5;

Qy	44	QEYWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPAS	103
		: :: :   :           :   :   :   :      :      :   :   :   :	
Db	58	OLKGLIVMLYSIVVVVGLVGNCLLVLVIARVRRLHNVTNFLIGNLALS DVL MCAACVPLT	117

Qy 104 LLVDI-TESWLFGHALCKVIPYLQAVSVSVAVLTSFIPIDRWYAICHPLLFKSTARRAR 162  
 | :||| || :: :|| |:| |:|| | :||: : ||| : : : :  
 Db 118 LAYAFEPRGWVFGGGLCHLVFFLQPVTYVSVFTLTTIAVDRYVVLVHPLRRRISLKLSA 177  
 Qy 163 GSILGIWAVSLAIMVPQAAVMQSSSVLPLEANRTRLFSLCHERW-ADDLYPKIYHSCFFI 221  
 ::|||||:| : :| | : | | | | : :||| : :||| :  
 Db 178 YAVLGIWALSAVLALPAAVHTYHVELKPHDVR-----LCEEFWGSQERQRQIYAWGLLL 231  
 Qy 222 VTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSLVRNWKRPSDQLGDLEQGLSGEPQPRGR 281  
 ||| || : ::| :|| | :||: :| :||| : :||| :  
 Db 232 GTYLLPPLLAILLSYVRVSVKLRNRVPGSQTQSQADWDR----- 270  
 Qy 282 AFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFT 341  
 ||:| :|||::|||||:||: :|:|: : :||| :  
 Db 271 -----ARRRTFCLVVVVVVFALCWPLHIFNLLR---DLDPRAIDPYAFGLVQL 318  
 Qy 342 FSHWLVYANSAANPIIYNFL 361  
 ||| ::| ||| :|  
 Db 319 LCHWLAMSSACYNPFIYAWL 338

### RESULT 3

I39187

neuropeptide Y/neuropeptide YY receptor Y2 - human

N;Alternate names: neuropeptide y/neuropeptide YY receptor type 2

C;Species: Homo sapiens (man)

C;Date: 01-Mar-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C;Accession: I39187; I39163; G02301

R;Gerald, C.; Walker, M.W.; Vaysse, P.J.

J. Biol. Chem. 270, 26758-26761, 1995

A;Title: Expression cloning and pharmacological characterization of a human hippocampal neuropeptide Y/neuropeptide YY Y2 receptor subtype.

A;Reference number: I39187; MUID:96070760; PMID:7592910

A;Accession: I39187

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-381 <GER>

A;Cross-references: UNIPROT:P49146; EMBL:U36269; NID:g1063633; PIDN: AAC50281.1; PID:g1063634

R;Rose, P.M.; Fernandes, P.; Lynch, J.S.; Frazier, S.T.; Fisher, S.M.; Kodukula, K.; Kienzle, B.; Seethala, R.

J. Biol. Chem. 270, 22661-22664, 1995

A;Title: Cloning and functional expression of a cDNA encoding a human type 2 neuropeptide Y receptor.

A;Reference number: I39163; MUID:96032678; PMID:7559383

A;Accession: I39163

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-133, 'A', 135-381 <ROS>

A;Cross-references: EMBL:U32500; NID:g1000750; PIDN: AAA93170.1; PID:g1000751

R;Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.

submitted to the EMBL Data Library, December 1995

A;Reference number: H01019

A;Accession: G02301

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA  
A;Residues: 1-171, 'G', 173, 'R', 175-201, 'P', 203-208, 'A', 210-381 <YAN>  
A;Cross-references: EMBL:U42389; NID:g1314329; PIDN:AAB07760.1; PID:g1314330  
C;Genetics:  
A;Gene: GDB:NPY2R  
A;Cross-references: GDB:4365607; OMIM:162642  
A;Map position: 4q31-4q31  
C;Superfamily: neuropeptidergic receptor  
C;Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester bond; transmembrane protein  
F;49-76/Domain: transmembrane #status predicted <TM1>  
F;87-113/Domain: transmembrane #status predicted <TM2>  
F;166-186/Domain: transmembrane #status predicted <TM4>  
F;221-237/Domain: transmembrane #status predicted <TM5>  
F;269-291/Domain: transmembrane #status predicted <TM6>  
F;305-328/Domain: transmembrane #status predicted <TM7>  
F;123-203/Disulfide bonds: #status predicted  
F;342/Binding site: palmitate (Cys) (covalent) #status predicted  
F;372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.2%; Score 392; DB 2; Length 381;  
Best Local Similarity 27.6%; Pred. No. 3.7e-26;  
Matches 101; Conservative 70; Mismatches 129; Indels 66; Gaps 9;

Qy	3 PSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVALV	62
	::      :   :       :: :: ::	
Db	24 PQTTPRGEL-----VPDPEPELI----DSTKLIEVQVVLILAYCSIILLGVI	66
Qy	63 GNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLCPASLLVDITESWLFHALCKVI	122
	:     :        :     ::  :   :   :  :        ::	
Db	67 GNSLVIHVVIKFKSMRTVTNFFIANLAVADLLVNTLCPLFTLTYTLMGEWKMGPVLCHLV	126
Qy	123 PYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARARSGSILGI-WAVSLAIMVPQAA	181
	::   :   :         :     ::   ::    :  :	
Db	127 PYAQGLAVQVSTITLTVIDLRHRCIVYHLESK-ISKRISFLIIGLAWGISALLASPLAI	185
Qy	182 VMQSS--SVLPELANRTRLFSLCHERWADD--LYPKIYHSCFFIVTYLAPLGLMAMAYF	236
	:   ::    :      :   :   ::   :    :::	
Db	186 FREYSLIEIIPDFE----IVACTEKWPGEEEKSIYGTVYSSLSSLLILYVLPLGIISFSYT	240
Qy	237 QIFRKWLGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKT	296
	: :	
Db	241 RIWSKLNHNVSPGA-----ANDHYHQRRQKT	266
Qy	297 AKMLMVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPI	356
	:   ::    :  :   :     :      :   ::     :	
Db	267 TKMLVCVVVVFAVSWLP---LHAFAQLAVIDSQVLDLKEYKLIFTVFHIIAMCSTFANPL	323
Qy	357 IYNFLS 362	
	:  :::	
Db	324 LYGMWN 329	

RESULT 4

S50150

gastric CCK-A receptor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Apr-2000  
C;Accession: S50150  
R;Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.  
Biochim. Biophys. Acta 1219, 321-327, 1994  
A;Title: Cloning and expression of the rabbit gastric CCK-A receptor.  
A;Reference number: S50150; MUID:95002144; PMID:7918628  
A;Accession: S50150  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-427 <REU>  
C;Superfamily: neurokinin 1 receptor

Query Match 20.2%; Score 392; DB 2; Length 427;  
Best Local Similarity 28.8%; Pred. No. 4.2e-26;  
Matches 110; Conservative 78; Mismatches 150; Indels 44; Gaps 11;

Qy	8	GAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEW--VLIAAYVAVFVVALVGN	64
	:         ::      :              : :::		
Db	9	GNASGIPPP-----PCELGLDNETLFCLDQP---PPSKIEWQPAVQILLYSLIFLLSVLGN	59

Qy	65	TLVCLAVWRNHHMRTVTNYFIVNLSADLVTAICLCPASLLVDITESWLFHALCKVITY	124
	:            ::: ::: ::: :::    :		
Db	60	TLVITVLIRNKRMRTVTNIFLLSLAISDLMLCLFCMPFNLPNLLKDFIFGSALCKTTTY	119

Qy	125	LQAVSVSVAVLTLSFIPLDRWYAICHPLLFK--STARRARGSILGIWAVSLAIMVPQAAV	182
	:           :		
Db	120	LMGTSVSVSTLNLAISLERYGAICKPLQSRVWQTSHALKVIAATWCLSFAIMTPYPIY	179

Qy	183	MQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKL	242
	:::  :		
Db	180	--SNLVPFTKTNNQTANMCRFLLPSDVMQQAWHTFLLLILFLIPGTIVMMVAYGMISEL	236

Qy	243	W-GRQIPGTT SALVRNWK-----RPSDQLGDLEQGLSGEPQPRGRA	282
	:   :   :		
Db	237	YQGIKFDASQKSAKERKASTGSGRFEDNDGCYLQRSKPTRQL-ELQQ-LSGGGGGRVSR	294

Qy	283	F--LAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLRVFGMFRQASDREAVYACF	340
	:   :		
Db	295	IHSSSSAAALMAKKRVIRMLMIVVLLFCWMPIFSANAWRAYDTV--SAERRLSGTPI	351

Qy	341	TFSHWLVYANSAANPIIYNFLS	362
	:       :		
Db	352	SFILLSSYTSSCVNPIIYCFMN	373

RESULT 5  
JC7809  
sulfakinin receptor protein, DSK-R1 - fruit fly (*Drosophila melanogaster*)  
C;Species: *Drosophila melanogaster*  
C;Date: 03-Jun-2002 #sequence\_revision 03-Jun-2002 #text\_change 09-Jul-2004  
C;Accession: JC7809  
R;Kubiak, T.M.; Larsen, M.J.; Burton, K.J.; Bannow, C.A.; Martin, R.A.;  
Zantello, M.R.; Lowery, D.E.  
Biochem. Biophys. Res. Commun. 291, 313-320, 2002  
A;Title: Cloning and functional expression of the first *Drosophila melanogaster*  
sulfakinin receptor DSK-R1.  
A;Reference number: JC7809; PMID:11846406; MUID:21835488

A;Accession: JC7809  
 A;Molecule type: mRNA  
 A;Residues: 1-584 <KUB>  
 A;Cross-references: UNIPROT:Q7M3J6; GB:AX128640  
 C;Comment: This receptor, the first functionally active orphan Drosophila sulfakinin G-protein-coupled receptor, with seven transmembrane domains, has the possible roles in insect brain and/or gut functions.  
 C;Genetics:  
 A;Gene: dsk-r1  
 A;Map position: 17  
 F;115-139/Domain: transmembrane region #status predicted <TMR1>  
 F;149-167/Domain: transmembrane region #status predicted <TMR2>  
 F;189-207/Domain: transmembrane region #status predicted <TMR3>  
 F;229-250/Domain: transmembrane region #status predicted <TMR4>  
 F;275-300/Domain: transmembrane region #status predicted <TMR5>  
 F;431-454/Domain: transmembrane region #status predicted <TMR6>  
 F;467-491/Domain: transmembrane region #status predicted <TMR7>  
  
 Query Match 20.0%; Score 388; DB 2; Length 584;  
 Best Local Similarity 26.1%; Pred. No. 1.3e-25;  
 Matches 118; Conservative 69; Mismatches 137; Indels 128; Gaps 15;  
  
 Qy 3 PSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVALV 62  
 ||::|| : | ||| | ||| : | : : ||| : ||| : : : ||| : ||| : : : ||| : ||| :  
 Db 96 PSSTPASSSSTSTG---MPV-----W-LIPSYSMILLFAVL 127  
  
 Qy 63 GNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCKVI 122  
 || || : :| ||||:||| :|||:|||: :|||:|||: :|||:|||: : :|||:|||: : :|||:  
 Db 128 GNLLVISTLVQNRRMRTITNVFLLNLAIISDMLLGVLCMPVTLVGTLLRNFIFGEFLCKLF 187  
  
 Qy 123 PYLQAVSVSVAVLTSFIPLDRWAICHPLLFKS--TARRARGSILGIWAVSLAIMVPQA 180  
 : || ||:|: ||| | :|||:||||| :| ||| | ||| : ||| : ||| : ||| : ||| :  
 Db 188 QFSQAASVAVSSWTI LVAISCERYYAICHPLRSRSWQTISHAYKIIGFIWLGGILCMTPIA 247  
  
 Qy 181 AVMQSSSVLPELANRTRL-FSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIF 239  
 | :| :| :| :| ||| | | | | | | :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 248 -----VFSQLIPTSRPGYCKCREFWPDQGYELFYNILLDFLLVPLLVLCVAYILIT 300  
  
 Qy 240 RKLW-----GRQI-----PGT-----TSALVRNWKRPSDL 265  
 | |: | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 301 RTLYVGMAKDSGRILQQSLPVSATAGGSAPNPGTSSSNICILVLTATAVYN-ENSNNNN 359  
  
 Qy 266 GDLEQGLSG-----EPQPRGRAFLA-----EV 287  
 | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 360 GNSEGSAGGGSTNMATTLLTRPTAPTVI TTTTTTVTLAKTSSPSIRVHDAALRRSNEA 419  
  
 Qy 288 KQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFG-MFRQASDREAVYACFTFSHWL 346  
 | : :| :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 420 KTLESKKRKKMLFVVLFEFFICWTPLYVINTMVMLIGPVVYEVYD---YTAISFLQLL 475  
  
 Qy 347 VYANSAANPIIYNFLS-----GLPW 366  
 | ::| | ||| | | :| | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 476 AYSSSSCCNPITYCFMNASFRRAFDTEKFGLPW 507

RESULT 6  
S17783

tachykinin receptor homolog DTKR - fruit fly (*Drosophila melanogaster*)  
C;Species: *Drosophila melanogaster*  
C;Date: 22-Nov-1996 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
C;Accession: S17783  
R;Li, X.J.; Wolfgang, W.; Wu, Y.N.; North, R.A.; Forte, M.  
EMBO J. 10, 3221-3229, 1991  
A;Title: Cloning, heterologous expression and developmental regulation of a *Drosophila* receptor for tachykinin-like peptides.  
A;Reference number: S17783; MUID:92007772; PMID:1717263  
A;Accession: S17783  
A;Molecule type: mRNA  
A;Residues: 1-519 <LIX>  
A;Cross-references: UNIPROT:P30975; EMBL:X62711; NID:g8505; PIDN:CAA44595.1;  
PID:g8506  
A;Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in  
lacking 481-Gly  
C;Genetics:  
A;Gene: FlyBase:Takr99D  
A;Cross-references: FlyBase:FBgn0004622  
C;Superfamily: neurokinin 1 receptor  
C;Keywords: G protein-coupled receptor; neurotransmitter receptor; transmembrane  
protein

A34916

neurokinin 3 receptor - rat

N;Alternate names: neuromedin K receptor; NK-3 receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004

C;Accession: A34916

R;Shigemoto, R.; Yokota, Y.; Tsuchida, K.; Nakanishi, S.

J. Biol. Chem. 265, 623-628, 1990

A;Title: Cloning and expression of a rat neuromedin K receptor cDNA.

A;Reference number: A34916; MUID:90110113; PMID:2153106

A;Accession: A34916

A;Molecule type: mRNA

A;Residues: 1-452 <SHI>

A;Cross-references: UNIPROT:P16177; GB:J05189; NID:g205670; PIDN:AAA41688.1;

PID:g205671

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 19.9%; Score 384.5; DB 2; Length 452;  
Best Local Similarity 28.2%; Pred. No. 2e-25;  
Matches 99; Conservative 64; Mismatches 133; Indels 55; Gaps 9;

Qy 11 MGVPPGSREPPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLA 70  
Db 45 LGLPATTQAPSQVRANLTNQFVQPSWRIAL-----WSL--AYGLVVAVAVFGNLIVIWI 96

Qy 71 VWRNHHMRTVTNYFIVNLSADLVTAICLPAASLLVDITESWLFGHALCKVIPYLNQAVSV 130  
Db 97 ILAHKRMRTVTNYFLVNLAESDASVAFNTLINFIYGLHSEWYFGANYCRFQNFFPITAV 156

Qy 131 SVAVLTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQAAVMQSSVLP 190  
Db 157 FASIYSMTAIAVDRYMAIIDPLKPRLSATATKIVIGSIWIЛАFLLAFPQ-CLYSKIKVMP 215

Qy 191 ELANRTRLFSLCHERWADDLYPK---IYHSCFFIVTYLAPIGLMAMAYFQIFRKLGGRQI 247  
Db 216 ---GRT----LCYVQWPEG--PKQHFTYHIIIVIILVYCFPLLIMGVTTIVGITLGGEI 266

Qy 248 PGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLVF 307  
Db 267 PGDT CDKYH-----EQLKAKRKVVKMMIIVVVTF 295

Qy 308 ALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAAANPIIY 358  
Db 296 AICWL PYH VY FILTAIYQQLN RWKYIQQVYLA---SFWLAMSSTMYNPIIY 343

RESULT 8

JQ1517

neurokinin 3 receptor - human

N;Alternate names: neuromedin K receptor; NK-3 receptor

C;Species: Homo sapiens (man)

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C;Accession: JQ1517; S20435; S21237

R;Huang, R.R.C.; Cheung, A.H.; Mazina, K.E.; Strader, C.D.; Fong, T.M.

Biochem. Biophys. Res. Commun. 184, 966-972, 1992

A;Title: cDNA sequence and heterologous expression of the human neurokinin-3 receptor.  
A;Reference number: JQ1517; MUID:92246993; PMID:1374246  
A;Accession: JQ1517  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-465 <HUA>  
A;Cross-references: UNIPROT:P29371; GB:M89473; NID:g189223; PIDN:AAA36366.1; PID:g189224  
A;Experimental source: brain  
R;Buell, G.; Schulz, M.F.; Arkinstall, S.J.; Maury, K.; Missotten, M.; Adami, N.; Talabot, F.; Kawashima, E.  
FEBS Lett. 299, 90-95, 1992  
A;Title: Molecular characterisation, expression and localisation of human neurokinin-3 receptor.  
A;Reference number: S20435; MUID:92183914; PMID:1312036  
A;Accession: S20435  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-2,'I',4-62,'R',64-465 <BUE>  
A;Cross-references: GB:S86392; NID:g246908; PIDN:AAB21706.1; PID:g246909  
R;Takahashi, K.; Tanaka, A.; Hara, M.; Nakanishi, S.  
Eur. J. Biochem. 204, 1025-1033, 1992  
A;Title: The primary structure and gene organization of human substance P and neuromedin K receptors.  
A;Reference number: S21188; MUID:92201186; PMID:1312928  
A;Accession: S21237  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-438,'F',440-465 <TAK>  
A;Cross-references: GB:X65172; NID:g35022; PIDN:CAA46291.1; PID:g825695  
C;Comment: The endogenous ligand of this receptor is neurokinin 3 (neuromedin K), one of the peptides in the mammalian tachykinin system.  
C;Genetics:  
A;Gene: GDB:TACR3  
A;Cross-references: GDB:9599126  
C;Superfamily: neurokinin 1 receptor  
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane protein  
F;83-111/Domain: transmembrane #status predicted <TM1>  
F;122-147/Domain: transmembrane #status predicted <TM2>  
F;160-181/Domain: transmembrane #status predicted <TM3>  
F;202-221/Domain: transmembrane #status predicted <TM4>  
F;247-272/Domain: transmembrane #status predicted <TM5>  
F;300-321/Domain: transmembrane #status predicted <TM6>  
F;333-355/ECmain: transmembrane #status predicted <TM7>  
F;23,50,73/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;158-233/Disulfide bonds: #status predicted

Query Match 19.8%; Score 384; DB 1; Length 465;  
Best Local Similarity 27.9%; Pred. No. 2.3e-25;  
Matches 100; Conservative 67; Mismatches 135; Indels 56; Gaps 10;

Qy 4 SATPGAQMVGPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVG 63  
|::| | :|:| | || : ::|:: || | | || || | ||:|  
Db 52 SSSPSA-LGLPVASPAPSQWPWANLTNQFVQPSWRIAL-----WSL--AYGVVVAVAVLG 102

Qy	64	NLTLCVLA   :   . : :       :     : :   . : : :        : .	123
Db	103	NLIVIWI 103 LAHKRMRTVTNYFLVNLA FSDASMAAFNLT LVNFIALHSEWYFGANYCRFQN	162
Qy	124	YLQAVSV : : : : .   :      : :       : :       : :     : .	183
Db	163	FFPITAVF ASIYSMTAIA VDRYMAIIDPLK PRLSATATKIVIGSI WILAFLLA FPQ-CLY	221
Qy	184	QSSSVLP ELANRTRLF SLCHERWADDLYPK --IYHSCFFIV TYLAPLGLMAMAY FQIFR	240
Db	222	SKTKVMP ---GRT ---LCFVQWP EG--PKQHFTY HIIVII LVYCFPLL IMGITYTIVGI	272
Qy	241	KLWGRQIP GTT SALVRN WKRP SDQLGD LEQGLSGEP QPRGRAFLAEV KQMRARRKTAKML	300
Db	273	TLWGGEIP GDTCDKYH ----- -----EQLAKR KVVKMM	301
Qy	301	MVVLLVF ALCYLP ISVLNV LKRVFGMFR QASDRE AVYACFT FSHWLVY ANSAA NPIIY	358
Db	302	IIVVM TFAICWL PYHIY FILTAI YQOLNR WKYI QQVYLA ---SF WLAMS STM YNPIIY	356

### RESULT 9

S55524

### neurokinin 3 receptor - mouse (fragment)

N;Alternate names: neuromedin K receptor; NK-3 receptor

C; Species: *Mus musculus* (house mouse)

C; Date: 01-Aug-1995 #sequence revision 01-Sep-1995 #text change 09-Jul-2004

C:Accession: S55524: I73045

R; Maroteaux, L.

submitted to the EMBL Data Library, June 1995

A: Reference number: S55524

A:Accession: S55524

A: Molecule type: mRNA

A:Residues: 1-385 <MAR>

#### A:Cross-references: INT

FID:ges1050  
B.Cook G.A

J. Inst. 152, 1929-1935, 1964.

J. Immunol. 152, 1830-1835, 1994  
© 1994 by The American Association of Immunologists

## A;Title: Molecular

## **schistosomiasis mansoni**

A;Reference number: 156216; MUID:94165478; PMID:81  
33-5732045

A;Accession: I73045

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A; Residues: 103-197, 'S

A;Cross-references: GB:L27827; NID:g450288; PIDN: 5450288

C; Superfamily: neurokinin 1 receptor

Best Local Similarity 28.2%; Pred. No. 5.5e-25;  
Matches 99; Conservative 63; Mismatches 134; Indels 55; Gaps 9;

Qy 11 MGVPPGSREPSPVPDYEDFLRLWRDYLKPQYEWVLIAAYVAVFVALVGNTLVCLA 70  
      :|:|| :|| | : ::||:: || | | | | | | | |:|| :|  
Pb 45 IGLI-PVTSOAPSOVRDNLTNOFVOPSWRITAL-----WSL--AYGIVVAVAVEGNLIIVIWI 96

## RESULT 10

JN0692

## cholecystokinin type A receptor - human

C; Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004

C;Accession: JN0692; JN0590

R;de Weerth, A.; Pisegna, J.R.; Huppi, K.; Wank, S.A.

Biochem. Biophys. Res. Commun. 194, 811-818, 1993

A;Title: Molecular cloning, functional expression and chromosomal localization of the human cholecystokinin type A receptor.

A; Reference number: JN0692; MUID:93343941; PMID:8343165

A;Accession: JN0692

A; Molecule type: mRNA

A; Residues: 1-428 <DEW>

A;Cross-references: UNIPROT:P32238; GB:L19315; NID:g306595; PIDN:AAA02819.1;  
PID:g306596

A;Experimental source: gallbladder  
R;Ulrich, C.D.; Ferber, I.; Holicky, E.; Hadac, E.; Buell, G.; Miller, L.J.  
Biochem. Biophys. Res. Commun. 193, 204-211, 1993

A;Title: Molecular cloning and functional expression of

### cholecystokinins A and B

A; Reference number: JN0590; MUID:93277552

A;Accession: JN0590

A; Status: nucleic acid

A;Molecule type: DNA

A;Residues: 1-428 <ULR>

A;Cross-references: GB:L13605; NID:g306490; PIDN:AAA35659.1; PID:g306491  
A;Experimental source: gallbladder  
C;Comment: This protein has diverse physiological roles in the gastrointestinal system where it mediates pancreatic growth and enzyme secretion, smooth muscle contraction of the gallbladder and stomach, and secretion from gastric mucosal cells.

cells.

### C: Genetics:

A;Gene: GDB:CCKRAR A;Gene: GDB:CCKRAR

A;Cross-references: GDB:141  
A;Map position: Anter Aftar

C;Superfamily: neurokinin 1 receptor  
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor;  
phosphoprotein; transmembrane protein  
F;40-67/Domain: transmembrane #status predicted <TM1>  
F;78-104/Domain: transmembrane #status predicted <TM2>  
F;116-137/Domain: transmembrane #status predicted <TM3>  
F;158-178/Domain: transmembrane #status predicted <TM4>  
F;208-234/Domain: transmembrane #status predicted <TM5>  
F;314-332/Domain: transmembrane #status predicted <TM6>  
F;350-369/Domain: transmembrane #status predicted <TM7>  
F;10,24,190,299/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;245,249,260,290/Binding site: phosphate (Ser) (covalent) (by protein kinase C)  
#status predicted  
F;256/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status  
predicted

Query Match 19.3%; Score 374.5; DB 2; Length 428;  
Best Local Similarity 28.3%; Pred. No. 1.4e-24;  
Matches 106; Conservative 76; Mismatches 155; Indels 37; Gaps 10;

QY 73 RNHHMRTVTNYFIVNLSLADVLVTAICLPA~~SLL~~DITESWLFGHALCKVIPYLQAVSVS 132  
|| | || || | :: : | : : | : : | : | : | : : | : | : | : | : | : | : | : |  
Ph 68 R~~N~~KDPMRTVTNYFIVNLSLADVLVTAICLPA~~SLL~~DITESWLFGHALCKVIPYLQAVSVS 132

Qy	191 ELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFRKLW----- 243
	: : ::   :   : : :     :   :      :   :
Pb	185 FTKNNNOTANMCREFLIPNDVMOOSWHTFLILLILETPTGIVMMVAYGLISLELYOGIKFEA 244

Qy 244 -----GRQIPGTTSA-----LVRNWKRPSDQLGDLEQGLSGEPQPRGR-AFLAEVK 288  
      : | ||| :                    ||  :| :| |  :|            |  :

Qy 289 QMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVY 348

Db 304 NLMAKKR VIRMLIVLIVVLFCLWMPIFSANAWR---AYDTASAERRLSGTPISFILLSY 360

Db 361 TSSCVNPIIYCFMN 374

RESULT 11

JC2459

### gastrin/cholecystokinin B receptor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 21-Feb-1995 #sequence revision 05-Apr-1995 #text change 09-Jul-2004

C:Accession: JC2459

R; Blandizzi, C.; Song, I.; Yamada, T.

R.Blandizzi, C., Song, T., Tamada, T.  
Biochem. Biophys. Res. Commun. 202, 947-953, 1994

A;Title: Molecular cloning and structural analysis of the rabbit gastrin/CCKB receptor gene.  
A;Reference number: JC2459; MUID:94324990; PMID:8048969  
A;Accession: JC2459  
A;Molecule type: mRNA  
A;Residues: 1-452 <BLA>  
A;Cross-references: UNIPROT:P46627; GB:L31548; NID:g495663; PIDN:AAA31194.1;  
PID:g495665  
C;Genetics:  
A;Introns: 49/1; 133/1; 216/2; 273/1  
C;Superfamily: neurokinin 1 receptor  
C;Keywords: receptor; transmembrane protein  
F;56-79/Domain: transmembrane #status predicted <TM1>  
F;85-104/Domain: transmembrane #status predicted <TM2>  
F;130-149/Domain: transmembrane #status predicted <TM3>  
F;169-187/Domain: transmembrane #status predicted <TM4>  
F;217-237/Domain: transmembrane #status predicted <TM5>  
F;339-359/Domain: transmembrane #status predicted <TM6>  
F;381-400/Domain: transmembrane #status predicted <TM7>

Query Match 19.3%; Score 373.5; DB 2; Length 452;  
Best Local Similarity 27.0%; Pred. No. 1.8e-24;  
Matches 99; Conservative 69; Mismatches 124; Indels 75; Gaps 9;

Qy	48	VLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNL	SLADVLVTAICL	PASLLVD	107				
	:	:   : :::    : : : :	::: ::: : :	:  :   :					
Db	54	IRVTLYAVIFLMSVGGNIL	IIVVLGLSRR	LRTVTNAFL	LSLAVSDL	LLAVACMPFT	LLPN	113	
Qy	108	ITESWLFGHALCKV	IPIYLQAVSVSVA	VLTLSFIPLDRWY	AICHPLL	FK--STARRARGSI	165		
	:	:::   :   :	:       : :        :	:					
Db	114	LMGTFIFGT	VICKAVSYLMGV	SVS	VSTLSLV	AIALERYS	AI	CRPLQARVWQTRSHAARVI	173
Qy	166	LGIWAVSLAIMVPQAAVMQSSSVLP	ELANRTRL	FSLCHERWADDLYPKIYHSCFF	YTVL	225			
		:   :	:		:  :  :				
Db	174	LATWL	LSGLLMVPYPVY	TAVQPVGPRV	LIQ-----CVHRWP	SARVRQTWSV	VL	LLLLLFF	226
Qy	226	APLGLMAMAYFQI	FRKLW-----	GRQIPGTT	TSALVRNWKR	P 261			
		:  :      : :							
Db	227	VPGVVMAVAYGLISRELY	LGRLFDSDSESQSRV	RQGG	LPGGAAPG-----P	275			
Qy	262	SDQLGDL--EQGLSGE	-----PQPRGRAFL	-----AEVKQM	RARR	294			
		:		:    : :					
Db	276	VHQNGRCRPEAGL	AGEDGDGCYVQL	PRSRPALE	LSALTAPISGPGP	PRPAQAK-LLAKK	334		
Qy	295	KTAKMLMVLLVFALCYLPISVLNV	LKRVFGMFRQASD	REAVYACFTFS	HVLVYANS	AAN 354			
	:	:  : :::  : : :	:	:       :					
Db	335	RVVRM	LLVIVVLF	MCWLPVYSANTWRA	FDG---PGA	HRALSGAPISFI	LLSYASACVN	391	
Qy	355	PIIYNFL	361						
		:    :							
Db	392	PLVYCFM	398						

RESULT 12

JQ1614

gastrin receptor - multimammate rat (Mastomys natalensis)

C;Species: Mastomys natalensis

C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C;Accession: JQ1614  
R;Nakata, H.; Matsui, T.; Ito, M.; Taniguchi, T.; Narabayashi, Y.; Arima, N.; Nakamura, A.; Kinoshita, Y.; Chihara, K.; Hosoda, S.; Chiba, T.  
Biochem. Biophys. Res. Commun. 187, 1151-1157, 1992  
A;Title: Cloning and characterization of gastrin receptor from ECL carcinoid tumor of Mastomys natalensis.  
A;Reference number: JQ1614; MUID:92412082; PMID:1530611  
A;Accession: JQ1614  
A;Molecule type: mRNA  
A;Residues: 1-450 <NAK>  
A;Cross-references: UNIPROT:P30796; GB:D12817; NID:g220646; PIDN:BAA02250.1;  
PID:g220647  
C;Superfamily: neurokinin 1 receptor  
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane protein  
F;59-83/Domain: transmembrane #status predicted <TM1>  
F;87-109/Domain: transmembrane #status predicted <TM2>  
F;132-150/Domain: transmembrane #status predicted <TM3>  
F;172-188/Domain: transmembrane #status predicted <TM4>  
F;216-243/Domain: transmembrane #status predicted <TM5>  
F;334-357/Domain: transmembrane #status predicted <TM6>  
F;380-398/Domain: transmembrane #status predicted <TM7>  
F;7,30,36/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.2%; Score 371.5; DB 2; Length 450;  
Best Local Similarity 28.8%; Pred. No. 2.6e-24;  
Matches 101; Conservative 67; Mismatches 136; Indels 47; Gaps 9;

Qy	48	VLIAAYVAVFVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVD	107
	:	: ::::     : : : : :       ::: ::: : :  :  :  :	
Db	56	IRITLYAVIFLMSIGGNMLIIVVLGLSRRRLRTVTNAFLSLAVSDLLLAVACMPFTLLPN	115
Qy	108	ITESWLFGHALCKVIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFK--STARRARGSI	165
	:	:::   :   :        :         :          :	
Db	116	LMGTFIFGTVICAKAVSYLMGVSVSSTNLVAIALERYSAICRPLQARVWQTRSHAARVI	175
Qy	166	LGIWAVSLAIMVPQAAVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYL	225
	:  :       :            : :		
Db	176	LATWLSSGLLMVPYPVYTVVQPGPRLQ-----CMHRWPSARVRQTVSLLMLFF	228
Qy	226	APLGLMAMAYFQIFRKWLW-GRQIPG---TTSALVRNW-----KRPSDQLGDLEQ-G	271
	:  :       : :   :         :		
Db	229	IPGVVMAVAYGLISRELYLGLRFDGNDNSDTQSRVRNQGGLPGGTAPGPVHQNGGCRHVT	288
Qy	272	LSGEPO-----PRGRAFL-----AEVKQMRARRKTAKMLMVLLVFALC	310
	::       :		
Db	289	VAGEDNDGCYVQLPRSRLLEMTTLTTPTPGPGLASANQAKLLAKRVRMMLLVIVLLFFLC	348
Qy	311	YLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNFL	361
	:         :       :		
Db	349	WLPIYSANTWCADF---PGAHRALSGAPISFIHLLSYASACVNPLVYCFM	396

RESULT 13

I59336

### galanin receptor 1 - human

C;Species: Homo sapiens (man)  
C;Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 09-Jul-2004  
C;Accession: I59336; JC5801; G01765; G02528  
R;Habert-Ortoli, E.; Amiranoff, B.; Loquet, I.; Laburthe, M.; Mayaux, J.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9780-9783, 1994  
A;Title: Molecular cloning of a functional human galanin receptor.  
A;Reference number: I59336; MUID:95024044; PMID:7524088  
A;Accession: I59336  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-349 <HAB>  
A;Cross-references: UNIPROT:P47211; GB:L34339; NID:g559047; PIDN:AAA50767.1;  
PID:g559048  
R;Lorimer, D.D.; Matkowskj, K.; Benya, R.V.  
Biochem. Biophys. Res. Commun. 241, 558-564, 1997  
A;Title: Cloning, chromosomal location, and transcriptional regulation of the  
human galanin-1 receptor gene (GALN1R).  
A;Reference number: JC5801; MUID:98086390; PMID:9425310  
A;Accession: JC5801  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-349 <LOR>  
A;Cross-references: GB:U53511; NID:g1297337; PIDN:AAC51936.1; PID:g1297338  
A;Note: submitted to the EMBL Data Library, April 1996  
R;Ross, P.C.  
submitted to the EMBL Data Library, March 1995  
A;Reference number: G08350  
A;Accession: G01765  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-14, 'W', 16-349 <ROS>  
A;Cross-references: EMBL:U23854; NID:g775209; PID:g775210  
C;Comment: This receptor inhibits cAMP formation, stimulates and inhibits  
phospholipase C activity, decreases phorbol ester-induced protein  
phosphorylation by a protein kinase C-independent mechanism, and increases  
arachadonic acid metabolism, as well as opens ATP-dependent K+ but closes N-type  
Ca2+ channels.  
C;Genetics:  
A;Gene: GDB:GALNR  
A;Cross-references: GDB:392699; OMIM:600377  
A;Map position: 18q23-18q23  
C;Superfamily: vertebrate rhodopsin

Query Match 19.2%; Score 371; DB 2; Length 349;  
Best Local Similarity 29.9%; Pred. No. 2.2e-24;  
Matches 97; Conservative 62; Mismatches 107; Indels 58; Gaps 10;

Qy 47 WVLIAAYVAVFVVALVGNTLVCLAVWRNH--HMRTVTNYFIVNLSLADVLVTAICLPA 104  
Db 34 FVTLVVFGLIFALGVLGNSLVTVLARSKPGKPRSTTNLFILNLSIADLAYLLFCIPFQA 93

Qy 105 LVDITESWLFGHALCKVIPYLQAVSVSVAVLTSFIPLDRWAICHPLLFKSTARRARGS 164  
Db 94 TVYALPTWVLGAFICKFIHYFFTWSMLVSIFTLAAMSDRYVAIVHSRR-SSSLRVSRNA 152

Qy 165 ILG---IWAVSLAIMVPQAAVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFI 221  
Db 156 TTYALPTWVLGAFICKFIHYFFTWSMLVSIFTLAAMSDRYVAIVHSRR-SSSLRVSRNA 212

## RESULT 14

I51898

## cholecystokinin A receptor - guinea pig

C; Species: *Cavia porcellus* (guinea pig)

C; Date: 04-Sep-1997 #sequence revision 04-Sep-1997 #text change 09-Jul-2004

C;Accession: I51898

R;De Weerth, A.; Piseagna, J.R.; Wank, S.A.

Am. J. Physiol. 265, G1116-G1121, 1993

A;Title: Guinea pig gallbladder and pancreas possess identical CCK-A receptor subtypes: receptor cloning and expression.

A: Reference number: T51898; MUID:94106629; PMTD:7916580

A:REFERENCE NUMBER:

A:Status: preliminary; translated from GB/EMBL/DDB-J

A:Seatus: preliminary  
A:Molecule type: mRNA

A: Residues: 1-430 <RES>

A;Residues: 1-450 <RES>  
A;Cross-references: UNIPROT:Q63931; GB:S68242; NID:g544723; PIDN:AAB29504.1;  
RTD:g544724

FID:9544724  
C:\Supoxfami

## C;superfamily: neuropeptide receptor

Query Match 19.1%; Score 370.5; DB 2; Length 430;  
 Best Local Similarity 27.4%; Pred. No. 3e-24;  
 Matches 104; Conservative 77; Mismatches 152; Indels 47; Gaps 10;

Qy 16 GSREPSPVPPDYEDEFRLRYLWRDYL PK-QYEW---VLIAAYVAVFVVVALVGNTLVCLAV 71  
|| | : || | | | | : | | | | : ; ; ; ; | : Pb 11 GSNITSACELGEENETLECLDR---PRPSKEWOPAVOILLYSLI ELLSVI GNTLVITV 66

Qy 72 WRNHHMRTVTNYFIVNLSLADVLVTAICLPA<sup>S</sup>LLVDITESWLF<sup>G</sup>H<sup>A</sup>LCKV<sup>I</sup>PY<sup>L</sup>QAVSVS 131

Db 67 IRNKRMRTVTNIFLSSLAVSDLMLCLFCMPFNLIPSLLKDFIFGSAVCKTTYFMGTSVS 126

DB 127 VSTFNLVAISLERYGAICKPLQSRVWQTSHALKVIAATWCLSFTIMTPYPIY---SNLV 183

QY 190 PELANRTLFLSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIIFRKWLW-GRQIP 248  
| | : ::| :| : :| : :|| | :| :|| | :| :| :

Db 184 PFTKNNNQTGNMCRFLLPNDVMQQTWHTFLLLILFLIPGIVMMVAYGLISLELYQGIKFD 243

Qy 249 GTTSALVRNWKRPSDLQGDLEQG---LSGEPQPGRGRAFLAEVKQ----- 289  
.: | : | :| | || |::|

Db 244 AIQKKSAKERKTSTGSSGPMEDSDGCYLQKSRHPR----KLELRQLSPSSSGSNRINRIR 299

Qy	290 -----MRARRKTAKMLMVLLFALCYLPISVNLKRVFGMFRQASDREAVYACFTF 342 :   :: :  : :::    ::     : : : ::  :
Db	300 SSSSTANLMAKKRVRIMLIVIVLFFLCWMPIFSANAWRAYDTV---SAERHLSGTPISF 356
Qy	343 SHWLVYANSAANPIIYNFLS 362     :         :
Db	357 TLLLSYTSSCVNPTLYCEFMN 376

RESULT 15

A44081

### **kappa-type opioid receptor - human**

C;Species: Homo sapiens (man)

C; Date: 27-Jun-1994 #sequence revision 27-Jun-1994 #text change 09-Jul-2004

C:Accession: A44081

R;Xie, G.X.; Miyajima, A.; Goldstein, A.

Proc. Natl. Acad. Sci. U.S.A. 89, 4124-4128, 1992

A;Title: Expression cloning of cDNA encoding a seven-helix receptor from human placenta with affinity for opioid ligands.

A: Reference number: A44081; MUD: 92237319; PMTD: 1315051

A:Accession: A44081

A: Status: preliminary

A: Molecule type: mRNA

A:Residues: 1-440 <XTE>

A;Cross-references: UNIPROT:P30098; GB:M84605; NID:g189391; PIDN:AAA36395.1;

PTD:g189392

C: Superfamily: neuropeptide receptor

**C:**Keywords: G protein-coupled receptor; transmembrane protein

Query Match . 19.1%; Score 370.5; DB 2; Length 440;  
Best Local Similarity 28.3%; Pred. No. 3.1e-24;  
Matches 106; Conservative 59; Mismatches 138; Indels 72; Gaps 12;

Qy 4 SATPAGAQMGVPP-----GSREPSPV-----PDYEDEFRLRYLWRDYLYPKQ 44  
          ||| ||| | ||| : ||| | | . ||| : | | |  
 Ph 9 SAVPGKNSWYRPRANLDPNITGGPAPTAASGCRPAHGSHTEGDRPGRGMVPELQDPLVNL 68

QY 45 YEWVLLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASL 104  
| | | | | ||::|| :| | : | |||||| |::||: || : |: | :

Qy 105 LVDITESWLFGHALCKVIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKFSTARRARGS 164

Qy 165 ILGIWAVSLAIMVPQAAVMQSSVLPLEANRTRLFSLCHERWADDLYPKI-YHSCFFIVT 223

Qy 224 YLAPLGLMAMAYFOI FRKLWGRQIPGTT SALVRNWKRP SDOLGDLEOGLSGEPOPRGRAF 283

Db 231 YCFPLLIMGITYTIVGITLWGGEIPGDTC-----DKYQ----- 263  
Cv 234 LALNWKDMDPDTVNMIDVLLWVNLGKPIGKLNLYLWDVNGMDFGLSPPENLWGTETG 263

Db 264 ----EQLKAKRKVVKKMIIIVVVTFAICWL PYHIYFILT A IYQQLN RWKYI QQVYLA--S 316

Qy            344 HWLVYANSAANPIIY 358  
              ||    ::::    |||||  
Db            317 FWLAMSSTMYNPIIY 331

Search completed: October 14, 2004, 10:56:56  
Job time : 21.6209 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2004, 10:55:56 ; Search time 68.6732 Seconds  
(without alignments)  
1737.280 Million cell updates/sec

Title: US-10-070-532-4

Perfect score: 1937

Sequence: 1 MEPSATPGAQMGVPPGSREP.....NSAANPIIYNFLSGLPWSLL 369

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result

Query

No.	Score	Match Length	DB	ID	Description
1	1937	100.0	369	10 US-09-393-696-4	Sequence 4, Appli
2	1909	98.6	369	13 US-10-077-874-4	Sequence 4, Appli
3	1875	96.8	389	9 US-09-828-538-20	Sequence 20, Appli
4	1875	96.8	389	10 US-09-211-823C-23	Sequence 23, Appli
5	1875	96.8	425	9 US-09-828-538-19	Sequence 19, Appli
6	1875	96.8	425	9 US-09-828-538-24	Sequence 24, Appli
7	1875	96.8	425	10 US-09-211-823C-22	Sequence 22, Appli
8	1875	96.8	425	14 US-10-225-567A-368	Sequence 368, App
9	1875	96.8	425	14 US-10-352-684A-22	Sequence 22, Appli
10	1874	96.7	402	10 US-09-393-696-2	Sequence 2, Appli
11	1872	96.6	372	10 US-09-393-696-6	Sequence 6, Appli
12	1872	96.6	372	13 US-10-077-874-6	Sequence 6, Appli
13	1870	96.5	425	10 US-09-826-509-549	Sequence 549, App
14	1869	96.5	402	13 US-10-077-874-2	Sequence 2, Appli
15	1869	96.5	425	9 US-09-961-848-2	Sequence 2, Appli
16	1755	90.6	427	9 US-09-730-931-2	Sequence 2, Appli
17	1326.5	68.5	460	14 US-10-081-810-46	Sequence 46, Appli
18	1313.5	67.8	444	10 US-09-992-331-19	Sequence 19, Appli
19	1313.5	67.8	444	14 US-10-081-810-45	Sequence 45, Appli
20	1313.5	67.8	444	14 US-10-225-567A-370	Sequence 370, App
21	1313.5	67.8	444	14 US-10-262-313-19	Sequence 19, Appli
22	1313.5	67.8	444	14 US-10-060-369-11	Sequence 11, Appli
23	1313.5	67.8	444	14 US-10-178-194-2	Sequence 2, Appli
24	1313.5	67.8	444	16 US-10-768-878-19	Sequence 19, Appli
25	1312.5	67.8	444	14 US-10-282-717-2	Sequence 2, Appli
26	1308.5	67.6	444	10 US-09-826-509-551	Sequence 551, App
27	1279	66.0	263	14 US-10-278-087A-54	Sequence 54, Appli
28	483.5	25.0	430	9 US-09-866-248A-8	Sequence 8, Appli
29	483.5	25.0	430	14 US-10-225-567A-658	Sequence 658, App
30	483.5	25.0	430	16 US-10-719-587-54	Sequence 54, Appli
31	483.5	25.0	441	14 US-10-292-798-890	Sequence 890, App
32	480.5	24.8	432	9 US-09-866-248A-2	Sequence 2, Appli
33	480.5	24.8	432	16 US-10-719-587-37	Sequence 37, Appli
34	479.5	24.8	428	9 US-09-292-973-4	Sequence 4, Appli
35	473.5	24.4	420	9 US-09-866-248A-6	Sequence 6, Appli
36	473.5	24.4	420	14 US-10-060-369-9	Sequence 9, Appli
37	473.5	24.4	522	14 US-10-081-810-53	Sequence 53, Appli
38	473.5	24.4	522	14 US-10-225-567A-512	Sequence 512, App
39	473.5	24.4	522	14 US-10-255-551-2	Sequence 2, Appli
40	473.5	24.4	522	15 US-10-072-012-360	Sequence 360, App
41	473.5	24.4	522	15 US-10-072-012-361	Sequence 361, App
42	473.5	24.4	522	15 US-10-276-774-2093	Sequence 2093, Ap
43	473.5	24.4	522	17 US-10-757-262-8	Sequence 8, Appli
44	467.5	24.1	417	15 US-10-072-012-358	Sequence 358, App
45	453	23.4	426	9 US-09-292-973-19	Sequence 19, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-393-696-4

; Sequence 4, Application US/09393696

; Publication No. US20030022277A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.  
; TITLE OF INVENTION: Human Neuropeptide Receptor  
; FILE REFERENCE: PF168P2  
; CURRENT APPLICATION NUMBER: US/09/393,696  
; CURRENT FILING DATE: 1999-09-10  
; EARLIER APPLICATION NUMBER: PCT/US95/05616  
; EARLIER FILING DATE: 1995-05-05  
; EARLIER APPLICATION NUMBER: US08/462,509  
; EARLIER FILING DATE: 1995-06-05  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 369  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-393-696-4

Query Match 100.0%; Score 1937; DB 10; Length 369;  
Best Local Similarity 100.0%; Pred. No. 1.7e-172;  
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSVPVDYEDFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQMGVPPGSREPSVPVDYEDFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
Qy	121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180
Qy	181 AVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db	181 AVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy	301 MVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Db	301 MVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Qy	361 LSGLPWSLL 369
Db	361 LSGLPWSLL 369

RESULT 2  
US-10-077-874-4  
; Sequence 4, Application US/10077874  
; Publication No. US20020115155A1  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel et al  
; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12  
;  
; CORRESPONDENCE ADDRESS:  
;  
; ADDRESSEE: Human Genome Sciences, Inc.  
;  
; STREET: 9410 Key West Avenue  
;  
; CITY: Rockville  
;  
; STATE: MD  
;  
; COUNTRY: USA  
;  
; ZIP: 20850  
;  
; COMPUTER READABLE FORM:  
;  
; MEDIUM TYPE: Floppy disk  
;  
; COMPUTER: IBM PC compatible  
;  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
;  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;  
; CURRENT APPLICATION DATA:  
;  
; APPLICATION NUMBER: US/10/077,874  
;  
; FILING DATE: 20-Feb-2002  
;  
; CLASSIFICATION: <Unknown>  
;  
; PRIOR APPLICATION DATA:  
;  
; APPLICATION NUMBER: 08/462,509  
;  
; FILING DATE: 05-JUNE-1995  
;  
; ATTORNEY/AGENT INFORMATION:  
;  
; NAME: Wales, Michele M.  
;  
; REGISTRATION NUMBER: 43,975  
;  
; REFERENCE/DOCKET NUMBER: PF168P1D1  
;  
; TELECOMMUNICATION INFORMATION:  
;  
; TELEPHONE: 301-309-8504  
;  
; TELEFAX: 301-309-8439  
;  
; INFORMATION FOR SEQ ID NO: 4:  
;  
; SEQUENCE CHARACTERISTICS:  
;  
; LENGTH: 369 amino acids  
;  
; TYPE: amino acid  
;  
; TOPOLOGY: linear  
;  
; MOLECULE TYPE: protein  
;  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-077-874-4

Query Match 98.6%; Score 1909; DB 13; Length 369;  
Best Local Similarity 98.6%; Pred. No. 7.1e-170;  
Matches 364; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARARRARGSILGIWAVSLAIMVPQA 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
||| : ||| ||| ||| ||| : | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLS E P Q P R G R A F L A E V K Q M R A R R K T A K M L 300  
Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
Qy 361 LSGLPWSLL 369  
Db 361 LSGLPWSLL 369

RESULT 3

US-09-828-538-20

; Sequence 20, Application US/09828538  
; Patent No. US20010025031A1  
; GENERAL INFORMATION:  
; APPLICANT: Ellis, Catherine E.  
; APPLICANT: Kwok, Cheni  
; APPLICANT: Bodsworth, Nicola J.  
; APPLICANT: Halsey, Wendy  
; APPLICANT: Van Horn, Stephanie  
; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods  
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications  
; FILE REFERENCE: GH-50038-C1  
; CURRENT APPLICATION NUMBER: US/09/828,538  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/088,624  
; PRIOR FILING DATE: 1998-06-08  
; PRIOR APPLICATION NUMBER: 60/093,726  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: 09/328,014  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 389  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS

US-09-828-538-20

Query Match 96.8%; Score 1875; DB 9; Length 389;  
Best Local Similarity 98.6%; Pred. No. 1.1e-166;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPG AQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYL YPKQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPG AQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYL YPKQYEWVLIAAYVAVFVVA 60  
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICL PASLLVDITESWLFGHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICL PASLLVDITESWLFGHALCK 120  
Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSI LGIWA VSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
|||:  
Db 181 AVMECSSVLPLEANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
  
Qy 241 KLWGRQIPGTTSAVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300  
|||:  
Db 241 KLWGRQIPGTTSAVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKAKML 300  
  
Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
|||:  
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
  
Qy 361 LSG 363  
|||:  
Db 361 LSG 363

RESULT 4

US-09-211-823C-23

; Sequence 23, Application US/09211823C  
; Publication No. US20030087801A1  
; GENERAL INFORMATION:  
; APPLICANT: HAGEN, JAMES JOSEPH  
; APPLICANT: TERRETT, JONATHAN ALEXANDER  
; APPLICANT: UPTON, NEIL  
; APPLICANT: PIPER, DAVID  
; APPLICANT: SMITH, MARTIN IAN  
; APPLICANT: KENNEDY, GUY ANTHONY  
; APPLICANT: PATEL, SARASWATI R.  
; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS  
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR  
; TITLE OF INVENTION: ANTAGONISTS THEREOF  
; FILE REFERENCE: P50745  
; CURRENT APPLICATION NUMBER: US/09/211,823C  
; CURRENT FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: US 60/069,459  
; PRIOR FILING DATE: 1997-12-15  
; PRIOR APPLICATION NUMBER: US 60/069,785  
; PRIOR FILING DATE: 1997-12-16  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 389  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS

US-09-211-823C-23

Query Match 96.8%; Score 1875; DB 10; Length 389;  
Best Local Similarity 98.6%; Pred. No. 1.1e-166;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVIAAYVAVFVVA 60  
|||:  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVIAAYVAVFVVA 60  
  
Qy 61 LVGNTLVCLAVWRNHMHRTVTNYFIVNLSLADVLVTAICLPAALLVDITESWLFGHALCK 120  
|||:

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120  
Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
||| : ||| ||| ||| ||| : | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300  
Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHVLVYANSAANPIIYNF 360  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHVLVYANSAANPIIYNF 360  
Qy 361 LSG 363  
|||  
Db 361 LSG 363

RESULT 5

US-09-828-538-19

; Sequence 19, Application US/09828538

; Patent No. US20010025031A1

; GENERAL INFORMATION:

; APPLICANT: Ellis, Catherine E.

; APPLICANT: Kwok, Cheni

; APPLICANT: Bodsworth, Nicola J.

; APPLICANT: Halsey, Wendy

; APPLICANT: Van Horn, Stephanie

; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods

; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications

; FILE REFERENCE: GH-50038-C1

; CURRENT APPLICATION NUMBER: US/09/828,538

; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/088,624

; PRIOR FILING DATE: 1998-06-08

; PRIOR APPLICATION NUMBER: 60/093,726

; PRIOR FILING DATE: 1998-07-22

; PRIOR APPLICATION NUMBER: 09/328,014

; PRIOR FILING DATE: 1999-06-08

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 19

; LENGTH: 425

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-828-538-19

Query Match 96.8%; Score 1875; DB 9; Length 425;

Best Local Similarity 98.6%; Pred. No. 1.3e-166;

Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

||||||||||||||||||||||||||||||||||||||||||||||  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVA 60  
  
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120  
||||||||||||||||||||||||||||||||||||||||||||||  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120  
  
Qy 121 VIPYLQAVSVSVAVTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
||||||||||||||||||||||||||||||||||||||||||||||  
Db 121 VIPYLQAVSVSVAVTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
  
Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
|||:|||||||||||||:||||||||||||||||||||||||||||||  
Db 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
  
Qy 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
||||||||||||||||||||||||||||||||||||||||||||||  
Db 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
  
Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
||||||||||||||||||||||||||||||||||||||||||||||  
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
  
Qy 361 LSG 363  
|||  
Db 361 LSG 363

## RESULT 6

US-09-828-538-24

; Sequence 24, Application US/09828538  
; Patent No. US20010025031A1  
; GENERAL INFORMATION:  
; APPLICANT: Ellis, Catherine E.  
; APPLICANT: Kwok, Cheni  
; APPLICANT: Bodsworth, Nicola J.  
; APPLICANT: Halsey, Wendy  
; APPLICANT: Van Horn, Stephanie  
; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods  
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications  
; FILE REFERENCE: GH-50038-C1  
; CURRENT APPLICATION NUMBER: US/09/828,538  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/088,624  
; PRIOR FILING DATE: 1998-06-08  
; PRIOR APPLICATION NUMBER: 60/093,726  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: 09/328,014  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-828-538-24

Query Match 96.8%; Score 1875; DB 9; Length 425;  
Best Local Similarity 98.6%; Pred. No. 1.3e-166;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120  
||||||||||||||||||||||||||||||||||||||||||||||||  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
||||||||||||||||||||||||||||||||||||||||||||  
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
|||:||||||||||||:||| ||||||||||||||||||||||||||  
Db 181 AVMECSSVLPPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
||||||||||||||||||||||||||||||||||||||||  
Db 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360  
||||||||||||||||||||||||||||||||||||||||  
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360

Qy 361 LSG 363  
|||  
Db 361 LSG 363

## RESULT 7

US-09-211-823C-22

; Sequence 22, Application US/09211823C

; Publication No. US20030087801A1

### ; GENERAL INFORMATION:

; APPLICANT: HAGEN, JAMES JOSEPH  
; APPLICANT: TERRETT, JONATHAN ALEXANDER  
; APPLICANT: UPTON, NEIL  
; APPLICANT: PIPER, DAVID  
; APPLICANT: SMITH, MARTIN IAN  
; APPLICANT: KENNEDY, GUY ANTHONY  
; APPLICANT: PATEL, SARASWATI R.

; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS  
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR  
; TITLE OF INVENTION: ANTAGONISTS THEREOF

; FILE REFERENCE: P50745  
; CURRENT APPLICATION NUMBER: US/09/211,823C  
; CURRENT FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: US 60/069,459  
; PRIOR FILING DATE: 1997-12-15  
; PRIOR APPLICATION NUMBER: US 60/069,785  
; PRIOR FILING DATE: 1997-12-16  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 22  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-211-823C-22

Query Match 96.8%; Score 1875; DB 10; Length 425;  
Best Local Similarity 98.6%; Pred. No. 1.3e-166;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60  
Db 1 MEPSATPGAQMVGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSVLPLEANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363  
Db 361 LSG 363

RESULT 8

US-10-225-567A-368

; Sequence 368, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED  
RECEPTORS (GPCRS)  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 368  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-368

Query Match 96.8%; Score 1875; DB 14; Length 425;  
Best Local Similarity 98.6%; Pred. No. 1.3e-166;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLWGRQIPGTTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363  
Db 361 LSG 363

#### RESULT 9

US-10-352-684A-22  
; Sequence 22, Application US/10352684A  
; Publication No. US20030215452A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals Inc.  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Healy, Aileen  
; APPLICANT: Weich, Nadine S.  
; APPLICANT: Kelly, Louise M.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303,  
13906,  
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,  
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847,  
1849,  
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES  
; FILE REFERENCE: MPI02-019P1RNOMNIM

; CURRENT APPLICATION NUMBER: US/10/352,684A  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: US 60/354,333  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: US 60/360,258  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/364,476  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/375,626  
; PRIOR FILING DATE: 2002-04-26  
; PRIOR APPLICATION NUMBER: US 60/386,494  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/390,965  
; PRIOR FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: US 60/392,480  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 60/394,128  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 60/399,783  
; PRIOR FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US 60/403,221  
; PRIOR FILING DATE: 2002-08-13  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: Homo Sapiens

US-10-352-684A-22

Query Match 96.8%; Score 1875; DB 14; Length 425;  
Best Local Similarity 98.6%; Pred. No. 1.3e-166;  
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLCPASLLVDITESWLFHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLCPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKFSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKFSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSLAVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLWGRQIPGTTSLAVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Db 301 MVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
Qy 361 LSG 363  
|||  
Db 361 LSG 363

RESULT 10

US-09-393-696-2

; Sequence 2, Application US/09393696  
; Publication No. US20030022277A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc. et al.  
; TITLE OF INVENTION: Human Neuropeptide Receptor  
; FILE REFERENCE: PF168P2  
; CURRENT APPLICATION NUMBER: US/09/393,696  
; CURRENT FILING DATE: 1999-09-10  
; EARLIER APPLICATION NUMBER: PCT/US95/05616  
; EARLIER FILING DATE: 1995-05-05  
; EARLIER APPLICATION NUMBER: US08/462,509  
; EARLIER FILING DATE: 1995-06-05  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 402  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-393-696-2

Query Match 96.7%; Score 1874; DB 10; Length 402;  
Best Local Similarity 98.3%; Pred. No. 1.5e-166;  
Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
|||  
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIPAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120  
|||  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSIILGIWAVSLAIMVPQA 180  
|||  
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSIILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAFLGLMAMAYFQIFR 240  
|||:  
Db 181 AVMECSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAFLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
|||  
Db 241 NLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
|||  
Db 301 MVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy        361 LSG 363  
          |||  
Db        361 LSG 363

## RESULT 11

US-09-393-696-6

; Sequence 6, Application US/09393696  
; Publication No. US20030022277A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc. et al.  
; TITLE OF INVENTION: Human Neuropeptide Receptor  
; FILE REFERENCE: PF168P2  
; CURRENT APPLICATION NUMBER: US/09/393,696  
; CURRENT FILING DATE: 1999-09-10  
; EARLIER APPLICATION NUMBER: PCT/US95/05616  
; EARLIER FILING DATE: 1995-05-05  
; EARLIER APPLICATION NUMBER: US08/462,509  
; EARLIER FILING DATE: 1995-06-05  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-393-696-6

Query Match            96.6%; Score 1872; DB 10; Length 372;  
Best Local Similarity    98.3%; Pred. No. 2.1e-166;  
Matches 357; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy        1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
          |||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||  
Db        1 MEPSATPGAQMGVPPGSRDPSVPDDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy        61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120  
          |||||||||||||||||  
Db        61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy        121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
          |||||||||||||  
Db        121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy        181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
          |||:|||||||||:|||||||||||||  
Db        181 AVMECSSVLPLEANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy        241 KLWGRQIPGTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
          |||||||||||||  
Db        241 KLWGRQIPGTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy        301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
          |||||||||||||  
Db        301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy        361 LSG 363  
          |||

Db 361 LSG 363

RESULT 12

US-10-077-874-6

; Sequence 6, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 372 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-077-874-6

Query Match 96.6%; Score 1872; DB 13; Length 372;

Best Local Similarity 98.3%; Pred. No. 2.1e-166;

Matches 357; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MEPSATPGAQMVGPPGSRDPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
 |||||||  
 Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
 |||||||  
 Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
 ||||:|||||  
 Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
 |||||||  
 Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
 |||||||  
 Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
 |||||||  
 Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
 |||||||  
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
 |||||||  
 Qy 361 LSG 363  
 |||  
 Db 361 LSG 363

#### RESULT 13

US-09-826-509-549

; Sequence 549, Application US/09826509  
 ; Publication No. US20030204073A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lehmann-Bruinsma, Karin  
 ; APPLICANT: Liaw, Chen W.  
 ; APPLICANT: Lin, I-Lin  
 ; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated  
 Known G  
 ; TITLE OF INVENTION: Protein-Coupled Receptors  
 ; FILE REFERENCE: AREN-207  
 ; CURRENT APPLICATION NUMBER: US/09/826,509  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/195,747  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: 09/170,496  
 ; PRIOR FILING DATE: 1998-10-13  
 ; NUMBER OF SEQ ID NOS: 589  
 ; SOFTWARE: PatentIn Version 2.1  
 ; SEQ ID NO 549  
 ; LENGTH: 425  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-09-826-509-549

Query Match 96.5%; Score 1870; DB 10; Length 425;  
 Best Local Similarity 98.3%; Pred. No. 3.7e-166;  
 Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
 |||||||  
 Db 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
 |||||||  
 Qy 61 LVGNTLVCLAWWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFGHALCK 120

Db ||||||| 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFGHALCK 120  
Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSSVLPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRTAKML 300  
Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRTKKML 300  
Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Qy 361 LSG 363  
Db 361 LSG 363

RESULT 14

US-10-077-874-2

; Sequence 2, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al  
; TITLE OF INVENTION: Human Neuropeptide Receptor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874  
; FILING DATE: 20-Feb-2002  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509  
; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.  
; REGISTRATION NUMBER: 43,975  
; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 402 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-077-874-2

Query Match 96.5%; Score 1869; DB 13; Length 402;  
Best Local Similarity 98.3%; Pred. No. 4.3e-166;  
Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60  
Db |||||||  
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120  
Db |||||||  
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120  
Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
Db |||||||  
Qy 181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db ||||:|||||:|||:|||||  
Qy 241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db |||||||  
Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
Db |||||||  
Qy 361 LSG 363  
Db |||  
Qy 361 LSG 363

RESULT 15

US-09-961-848-2

; Sequence 2, Application US/09961848  
; Patent No. US20020146719A1  
; GENERAL INFORMATION:  
; APPLICANT: Berglind Ran Olafsdottir  
; APPLICANT: Jeffrey Gulcher  
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE  
; FILE REFERENCE: 2345.1005-004  
; CURRENT APPLICATION NUMBER: US/09/961,848  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 09/479,128  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/379,083

; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-961-848-2

Query Match 96.5%; Score 1869; DB 9; Length 425;  
Best Local Similarity 98.3%; Pred. No. 4.6e-166;  
Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLYWRDYLKPQYEWVLIAAYVAVFVVA 60  
Db 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLYWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120  
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180  
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
Db 181 AVMECSSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
Db 241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360  
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363  
Db 361 LSG 363

Search completed: October 14, 2004, 11:16:35

Job time : 69.6732 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2004, 10:41:50 ; Search time 96.8388 Seconds  
(without alignments)  
2192.441 Million cell updates/sec

Title: US-10-070-532-4

Perfect score: 1937

Sequence: 1 MEPSATPGAQMGVPPGSREP.....NSAANPIIYNFLSGLPWSLL 369

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Score	Query Match	Length	DB ID	Description
1	1875	96.8	425	1 OX1R_HUMAN	O43613 homo sapien
2	1869	96.5	425	2 Q9HBV6	Q9hbv6 homo sapien
3	1755	90.6	416	1 OX1R_RAT	P56718 rattus norv
4	1753	90.5	416	2 Q6VNS3	Q6vns3 mus musculu
5	1753	90.5	416	2 AAR01326	Aar01326 mus muscu
6	1326.5	68.5	460	1 OX2R_RAT	P56719 rattus norv
7	1319.5	68.1	444	1 OX2R_CANFA	Q9tup7 canis famil
8	1315.5	67.9	443	2 Q6VLX3	Q6vlx3 mus musculu
9	1315.5	67.9	443	2 AAR01327	Aar01327 mus muscu
10	1315.5	67.9	443	2 AAR11294	Aar11294 mus muscu
11	1315.5	67.9	460	1 OX2R_MOUSE	P58308 mus musculu
12	1315.5	67.9	460	2 AAR01328	Aar01328 mus muscu
13	1315.5	67.9	460	2 AAR11293	Aar11293 mus muscu
14	1313.5	67.8	444	1 OX2R_HUMAN	O43614 homo sapien
15	1313.5	67.8	444	2 AAG28021	Aag28021 homo sapi

16	1257	64.9	364	2	Q8BV78	Q8bv78 mus musculu
17	1099	56.7	260	1	OX1R_MOUSE	P58307 mus musculu
18	945	48.8	199	2	Q80T45	Q80t45 mus musculu
19	654.5	33.8	166	2	Q8MJ13	Q8mj13 ovis aries
20	591	30.5	127	2	Q8SPR4	Q8spr4 ovis aries
21	510	26.3	109	2	Q8I010	Q8i010 bos taurus
22	483.5	25.0	430	1	NFF1_HUMAN	Q9gzq6 homo sapien
23	480.5	24.8	432	1	NFF1_RAT	Q9ep86 rattus norv
24	480	24.8	417	1	NFF2_MOUSE	Q924h0 mus musculu
25	476.5	24.6	405	2	Q924N0	Q924n0 mus musculu
26	473.5	24.4	522	1	NFF2_HUMAN	Q9y5x5 homo sapien
27	467.5	24.1	417	1	NFF2_RAT	Q9eqd2 rattus norv
28	457	23.6	399	2	Q75XU5	Q75xu5 gallus gall
29	457	23.6	399	2	BAC87782	Bac87782 gallus ga
30	453	23.4	432	2	Q924G9	Q924g9 rattus norv
31	444.5	22.9	758	2	Q7YU49	Q7yu49 drosophila
32	427.5	22.1	464	2	Q9VB87	Q9vb87 drosophila
33	427.5	22.1	464	2	AAF56655	Aaf56655 drosophil
34	422.5	21.8	449	1	NYR_DROME	P25931 drosophila
35	422	21.8	353	2	Q7PRC5	Q7prc5 anopheles g
36	415	21.4	370	2	Q6VMN6	Q6vmn6 mus musculu
37	415	21.4	370	2	AAQ84215	Aaq84215 mus muscu
38	412.5	21.3	375	2	O57463	O57463 brachydanio
39	411.5	21.2	370	1	GP10_RAT	Q64121 rattus norv
40	411	21.2	370	1	GP10_HUMAN	P49683 homo sapien
41	409	21.1	86	1	OX1R_PIG	O97661 sus scrofa
42	406	21.0	517	2	Q9VWR3	Q9vwr3 drosophila
43	406	21.0	598	2	Q9VWQ9	Q9vwq9 drosophila
44	403.5	20.8	542	2	Q9VRM0	Q9vrm0 drosophila
45	403.5	20.8	542	2	AAF50775	Aaf50775 drosophil

## ALIGNMENTS

### RESULT 1

#### OX1R\_HUMAN

ID OX1R\_HUMAN STANDARD; PRT; 425 AA.  
 AC O43613;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1).  
 GN Name=HCRTR1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98150861; PubMed=9491897;  
 RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,  
 RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,  
 RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,  
 RA McNulty D.E., Liu W.-S., Terrell J.A., Elshourbagy N.A., Bergsma D.J.,  
 RA Yanagisawa M.;  
 RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides

RT and G protein-coupled receptors that regulate feeding behavior.";  
RL Cell 92:573-585(1998).  
RN [2]  
RP REVIEW.  
RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;  
RA Hungs M., Mignot E.;  
RT "Hypocretin/orexin, sleep and narcolepsy.";  
RL Bioessays 23:397-408(2001).  
RN [3]  
RP REVIEW.  
RX MEDLINE=21178476; PubMed=11283317;  
RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;  
RT "To eat or to sleep? Orexin in the regulation of feeding and  
RT wakefulness.";  
RL Annu. Rev. Neurosci. 24:429-458(2001).  
CC -!-- FUNCTION: Moderately selective excitatory receptor for orexin-A  
CC and, with a lower affinity, for orexin-B neuropeptide. Seems to be  
CC exclusively coupled to the G(q) subclass of heteromeric G  
CC proteins, which activates the phospholipase C mediated signaling  
CC cascade (By similarity).  
CC -!-- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!-- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF041243; AAC39601.1; -.  
DR Genew; HGNC:4848; HCRTR1.  
DR MIM; 602392; -.  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
DR GO; GO:0007631; P:feeding behavior; TAS.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
DR GO; GO:0007268; P:synaptic transmission; TAS.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR000204; Orexin\_receptor.  
DR InterPro; IPR004059; Orexin\_receptor1.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRRHODOPSN.  
DR PRINTS; PR01521; OREXIN1R.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane.  
FT DOMAIN 1 46 Extracellular (Potential).  
FT TRANSMEM 47 67 1 (Potential).  
FT DOMAIN 68 80 Cytoplasmic (Potential).  
FT TRANSMEM 81 102 2 (Potential).  
FT DOMAIN 103 119 Extracellular (Potential).  
FT TRANSMEM 120 142 3 (Potential).  
FT DOMAIN 143 164 Cytoplasmic (Potential).  
FT TRANSMEM 165 185 4 (Potential).  
FT DOMAIN 186 216 Extracellular (Potential).

FT TRANSMEM 217 239 5 (Potential).  
 FT DOMAIN 240 298 Cytoplasmic (Potential).  
 FT TRANSMEM 299 321 6 (Potential).  
 FT DOMAIN 322 336 Extracellular (Potential).  
 FT TRANSMEM 337 360 7 (Potential).  
 FT DOMAIN 361 425 Cytoplasmic (Potential).  
 FT CARBOHYD 194 194 N-linked (GlcNAc. . .) (Potential).  
 SQ SEQUENCE 425 AA; 47521 MW; 1634083DE10CA092 CRC64;

Query Match 96.8%; Score 1875; DB 1; Length 425;  
 Best Local Similarity 98.6%; Pred. No. 1.5e-120;  
 Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLWRDYLYPKQYEWVLIAAYVAVFVA 60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLWRDYLYPKQYEWVLIAAYVAVFVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFGHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFGHALCK 120
Qy	121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180
Qy	181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
	:             :
Db	181 AVMECSSSVLPPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLWGRQIPGTTTSALVRNWKPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KLWGRQIPGTTTSALVRNWKPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

## RESULT 2

Q9HBV6  
 ID Q9HBV6 PRELIMINARY; PRT; 425 AA.  
 AC Q9HBV6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypocretin receptor-1 (Orexin receptor 1).  
 GN Name=HCRTTR1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=20429525; PubMed=10973318;  
RA Peyron C., Faáaco J., Rogers W., Ripley B., Overeem S., Charnay Y.,  
RA Nevsimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,  
RA Pedrazzoli M., Padigaru M., Kucherlapati M., Fan J., Maki R.,  
RA Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;  
RT "A mutation in a case of early onset narcolepsy and a generalized  
RT absence of hypocretin peptides in human narcoleptic brains.";  
RL Nat. Med. 6:991-997(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21580342; PubMed=11723285;  
RA Olafsdottir B.R., Rye D.B., Scammell T.E., Matheson J.K.,  
RA Stefansson K., Gulcher J.R.;  
RT "Polymorphisms in hypocretin/orexin pathway genes and narcolepsy.";  
RL Neurology 57:1896-1899(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Olafsdottir B.R., Stefansdottir R.H., Sigurdsson A., Hannesson H.H.,  
RA Sainz J., Scammell T.E., Stefansson K., Gulcher J.R.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Yeager M., Welch R., Haque K., Bergen A.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pooled tissue;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pooled tissue;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF202084; AAG28020.1; -.  
DR EMBL; AF202078; AAG28020.1; JOINED.  
DR EMBL; AF202079; AAG28020.1; JOINED.  
DR EMBL; AF202081; AAG28020.1; JOINED.

DR EMBL; AF202083; AAG28020.1; JOINED.  
 DR EMBL; AF202082; AAG28020.1; JOINED.  
 DR EMBL; AF202080; AAG28020.1; JOINED.  
 DR EMBL; AY062030; AAL47214.1; -.  
 DR EMBL; AY070269; AAL50221.1; -.  
 DR EMBL; BC074796; AAH74796.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016499; F:orexin receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR000204; Orexin\_receptor.  
 DR InterPro; IPR004059; Orexin\_receptorl.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PRINTS; PR01521; OREXIN1R.  
 DR PRINTS; PR01064; OREXINR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 425 AA; 47535 MW; B650B37F3A2CA096 CRC64;

Query Match 96.5%; Score 1869; DB 2; Length 425;  
 Best Local Similarity 98.3%; Pred. No. 3.9e-120;  
 Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPA	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPA	120
Qy	121	VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSI	180
Db	121	VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSI	180
Qy	181	AVMQSSSVLP	240
	:		
Db	181	AVMECSSVLP	240
Qy	241	KLWGRQIPGTT	300
Db	241	KLWGRQIPGTT	300
Qy	301	MVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWL	360
Db	301	MVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWL	360
Qy	361	LSG	363
Db	361	LSG	363

RESULT 3

OX1R\_RAT

ID OX1R\_RAT STANDARD; PRT; 416 AA.

AC P56718;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1).

GN Name=Hcrtr1;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=98150861; PubMed=9491897;

RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M., Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S., Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S., McNulty D.E., Liu W.-S., Terrell J.A., Elshourbagy N.A., Bergsma D.J., Yanagisawa M.;

RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides and G protein-coupled receptors that regulate feeding behavior.";

RL Cell 92:573-585(1998).

RN [2]

RP REVIEW.

RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;

RA Hungs M., Mignot E.;

RT "Hypocretin/orexin, sleep and narcolepsy.";

RL Bioessays 23:397-408(2001).

RN [3]

RP REVIEW.

RX MEDLINE=21178476; PubMed=11283317;

RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;

RT "To eat or to sleep? Orexin in the regulation of feeding and wakefulness.";

RL Annu. Rev. Neurosci. 24:429-458(2001).

CC -!- FUNCTION: Moderately selective excitatory receptor for orexin-A and, with a lower affinity, for orexin-B neuropeptide. Seems to be exclusively coupled to the G(q) subclass of heteromeric G proteins, which activates the phospholipase C mediated signaling cascade.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Highly expressed in the brain in the prefrontal cortex, hippocampus, paraventricular thalamus, ventromedial hypothalamus, arcuate nucleus, dorsal raphe nucleus, and locus coeruleus. Not detected in the spleen, lung, liver, skeletal muscle, kidney and testis. Orexin receptor mRNA expression has also been reported in the adrenal gland, enteric nervous system, and pancreas.

CC -!- INDUCTION: By nutritional state, up-regulated by fasting.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL; AF041244; AAC40041.1; -.

DR RGD; 2787; Hcrtr1.

DR InterPro; IPR000276; GPCR\_Rhodpsn.

DR InterPro; IPR000204; Orexin\_receptor.

DR InterPro; IPR004059; Orexin\_receptor1.

DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PRO0237; GPCRRHODOPSN.

DR PRINTS; PRO1521; OREXIN1R.

DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.

DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane.

FT DOMAIN 1 46 Extracellular (Potential).

FT TRANSMEM 47 67 1 (Potential).

FT DOMAIN 68 80 Cytoplasmic (Potential).

FT TRANSMEM 81 102 2 (Potential).

FT DOMAIN 103 119 Extracellular (Potential).

FT TRANSMEM 120 142 3 (Potential).

FT DOMAIN 143 164 Cytoplasmic (Potential).

FT TRANSMEM 165 185 4 (Potential).

FT DOMAIN 186 216 Extracellular (Potential).

FT TRANSMEM 217 239 5 (Potential).

FT DOMAIN 240 298 Cytoplasmic (Potential).

FT TRANSMEM 299 321 6 (Potential).

FT DOMAIN 322 336 Extracellular (Potential).

FT TRANSMEM 337 360 7 (Potential).

FT DOMAIN 361 416 Cytoplasmic (Potential).

FT CARBOHYD 194 194 N-linked (GlcNAc. . .) (Potential).

SQ SEQUENCE 416 AA; 46799 MW; 774DE7A22EA05D18 CRC64;

Query Match 90.6%; Score 1755; DB 1; Length 416;

Best Local Similarity 92.6%; Pred. No. 2.5e-112;

Matches 336; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60  
||| ||||||| ||| | || :||||||||| ||| ||| ||| ||| ||| :|||

Db 1 MEPSATPGAQPGVPTSSGEFPHLPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFLIA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPPASLLVDITESWLFGHALCK 120  
||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVAVTLSFIPLDRWAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :|||

Db 121 VIPYLQAVSVSVAVTLSFIPLDRWAICHPLLFKSTARRARGSILGIWAVSLAVMVPQA 180

Qy 181 AVMQSSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240  
||| :||| ||| ||| ||| :||| ||| :||| ||| ||| ||| ||| ||| ||| |||

Db 181 AVMECSSVLPLEANRTRLFSCDERWADELYPKIYHSCFFFVTLAPLGLMGMAFQIFR 240

Qy 241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300  
||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 KLWGPQIPGTTTSALVRNWKRPSQLEAQHQGLCTEPQPRARAFLAEVKQMRARRKTAKML 300

QY 301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
 |||||||  
 Db 301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
 |||  
 QY 361 LSG 363  
 |||  
 Db 361 LSG 363

#### RESULT 4

Q6VNS3

ID Q6VNS3 PRELIMINARY; PRT; 416 AA.  
 AC Q6VNS3;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Orexin receptor type-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Chen J., Randeva H.S.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY336083; AAR01326.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR000204; Orexin\_receptor.  
 DR InterPro; IPR004059; Orexin\_receptor1.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PRINTS; PR01521; OREXIN1R.  
 DR PRINTS; PR01064; OREXINR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 416 AA; 46766 MW; A8958C594C365E00 CRC64;

Query Match 90.5%; Score 1753; DB 2; Length 416;  
 Best Local Similarity 92.6%; Pred. No. 3.4e-112;  
 Matches 336; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVA 60  
 ||||||| :||| :|||||:  
 Db 1 MEPSATPGAQPGVPTSSGEFPHLPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFLIA 60  
 ||||||| :|||:  
 QY 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120  
 ||||||| :|||:  
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFQALCK 120  
 ||||||| :|||:  
 QY 121 VIPYLQAVSVSVAVLTLIFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180  
 ||||||| :|||:  
 Db 121 VIPYLQAVSVSVAVLTLIFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAVMVPQA 180  
 ||||||| :|||:  
 QY 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFR 240

```

Db      |||:||||||||||||||:| | |||:||||||||||||||| ||||| |
181 AVMECSSVLPLEANRTRLFSVCDEHWAELYPKIYHSCFFIVTYLAPLGLMGAMAYFQIFR 240

Qy      241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300
Db      241 KLWGRQIPGTT SALVRNWKRP SEQLEAQHQGLCTEPQPRARAFLAEVKQMRARRKTA KML 300

Qy      301 MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db      301 MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy      361 LSG 363
Db      361 LSG 363

```

#### RESULT 5

AAR01326

ID AAR01326 PRELIMINARY; PRT; 416 AA.  
AC AAR01326;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Orexin receptor type-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Chen J., Randeva H.S.;  
RT "Cloning and Characterization of the Mouse Type-1 Orexin Receptor  
(OX1R).";  
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY336083; AAR01326.1; -.  
KW Receptor.  
SQ SEQUENCE 416 AA; 46766 MW; A8958C594C365E00 CRC64;

Query Match 90.5%; Score 1753; DB 2; Length 416;  
Best Local Similarity 92.6%; Pred. No. 3.4e-112;  
Matches 336; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

```

Qy      1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60
Db      1 MEPSATPGAQPVGPTSSGEFPHLPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFLIA 60

Qy      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFGHALCK 120
Db      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFGQALCK 120

Qy      121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180
Db      121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAVMVPQA 180

Qy      181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db      181 AVMQSSVLPLEANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

```

Db 181 AVMECSSVLPLEANRTRLFSVCDEHWADELYPKIYHSCFFIVTYLAPLGLMGMAFQIFR 240  
 Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300  
 |||||||:||| ||| ||| ||| ||| |||  
 Db 241 KLWGRQIPGTT SALVRNWKRP SEQLEAQHQGLCTEPQPRARAFLAEVKQMRARRKTA KML 300  
 Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
 ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360  
 Qy 361 LSG 363  
 |||  
 Db 361 LSG 363

#### RESULT 6

OX2R\_RAT

ID OX2R\_RAT STANDARD; PRT; 460 AA.  
 AC P56719;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).  
 GN Name=Hcrtr2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=98150861; PubMed=9491897;  
 RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,  
 RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,  
 RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,  
 RA McNulty D.E., Liu W.-S., Terrell J.A., Elshourbagy N.A., Bergsma D.J.,  
 RA Yanagisawa M.;  
 RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides  
 RT and G protein-coupled receptors that regulate feeding behavior.";  
 RL Cell 92:573-585(1998).  
 RN [2]  
 RP REVIEW.  
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;  
 RA Hungs M., Mignot E.;  
 RT "Hypocretin/orexin, sleep and narcolepsy.";  
 RL Bioessays 23:397-408(2001).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=21178476; PubMed=11283317;  
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;  
 RT "To eat or to sleep? Orexin in the regulation of feeding and  
 RT wakefulness.";  
 RL Annu. Rev. Neurosci. 24:429-458(2001).  
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A  
 CC and orexin-B neuropeptides.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed in the brain in the cerebral cortex,

CC septal nuclei, hippocampus, medial thalamic groups, dorsal and  
CC median raphe nuclei, and many hypothalamic nuclei including the  
CC tuberomammillary nucleus, dorsomedial hypothalamus,  
CC paraventricular hypothalamic nucleus, and ventral premammillary  
CC nucleus. Not detected in the spleen, lung, liver, skeletal muscle,  
CC kidney and testis. Orexin receptor mRNA expression has also been  
CC reported in the adrenal gland, enteric nervous system, and  
CC pancreas.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; AF041246; AAC40042.1; -.

DR RGD; 2788; Hcrtr2.

DR InterPro; IPR000276; GPCR\_Rhodpsn.

DR InterPro; IPR000204; Orexin\_receptor.

DR InterPro; IPR004060; Orexin\_receptor2.

DR Pfam; PF00001; 7tm\_1; 1.

DR Pfam; PF03827; Orexin\_rec2; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PRINTS; PR01522; OREXIN2R.

DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.

DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.

KW G-protein coupled receptor; Glycoprotein; Transmembrane.

FT DOMAIN 1 54 Extracellular (Potential).

FT TRANSMEM 55 75 1 (Potential).

FT DOMAIN 76 88 Cytoplasmic (Potential).

FT TRANSMEM 89 110 2 (Potential).

FT DOMAIN 111 127 Extracellular (Potential).

FT TRANSMEM 128 150 3 (Potential).

FT DOMAIN 151 172 Cytoplasmic (Potential).

FT TRANSMEM 173 193 4 (Potential).

FT DOMAIN 194 224 Extracellular (Potential).

FT TRANSMEM 225 247 5 (Potential).

FT DOMAIN 248 304 Cytoplasmic (Potential).

FT TRANSMEM 305 327 6 (Potential).

FT DOMAIN 328 342 Extracellular (Potential).

FT TRANSMEM 343 366 7 (Potential).

FT DOMAIN 367 460 Cytoplasmic (Potential).

FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).

SQ SEQUENCE 460 AA; 52489 MW; 3B44E3D82F8B85D5 CRC64;

Query Match 68.5%; Score 1326.5; DB 1; Length 460;  
Best Local Similarity 70.9%; Pred. No. 6.1e-83;  
Matches 253; Conservative 39; Mismatches 44; Indels 21; Gaps 4;

Qy 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75  
::|| | ||:| |||||||:||:||:||| ||| |: |||||||:|| | ||:|||:||

Db 24 TQEPEFLNPTDYDDEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy : 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCKVIPYLQAVSVSVAL 135  
 |||||||:|||||||:|||||:|||||:|| :|||||||:|||:|||:  
 Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVAL 143  
 ||| | |||:|||:|||:|||:|||:|||:|||:|||:  
 Qy : 136 TLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQAAMQSSSVLPELANR 195  
 ||| | |||:|||:|||:|||:|||:|||:|||:  
 Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNSIVVIWIVSCIIMIPQAIVMERSSMLPGLANK 203  
 |||:|||:|||:|||:|||:|||:|||:  
 Qy : 196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLWGRQIPGTTSALV 255  
 |||:|||:|||:|||:|||:|||:|||:|||:  
 Db 204 TTLFTVCDERWGGEVYPKMYHICFLVTYMAPLCLMVLAYLQIFRKWLWCRQIPGTSSVVQ 263  
 |||:|||:|||:|||:  
 Qy : 256 RNWKRPSPDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306  
 |||:|||:|||:|||:  
 Db 264 RKWKQP-----QPVS---QPRGSGQQSKARIISAVAAEIKQIRARRKTARMLMVLLV 312  
 |||:|||:  
 Qy : 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363  
 |||:|||:  
 Db 313 FAICYLPISILNVLKRVFGMFTHTEDRETVDWFTFSHWLVYANSAANPIIYNFLSG 369

#### RESULT 7

##### OX2R\_CANFA

ID OX2R\_CANFA STANDARD; PRT; 444 AA.  
 AC Q9TUP7;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).  
 GN Name=HCRT2;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99385793; PubMed=10458611;  
 RA Lin L., Faraco J., Li R., Kadotani H., Rogers W., Lin X., Qiu X.,  
 RA de Jong P.J., Nishino S., Mignot E.;  
 RT "The sleep disorder canine narcolepsy is caused by a mutation in the  
 RT hypocretin receptor 2 gene.";  
 RL Cell 98:365-376(1999).  
 RN [2]  
 RP REVIEW.  
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;  
 RA Hungs M., Mignot E.;  
 RT "Hypocretin/orexin, sleep and narcolepsy.";  
 RL Bioessays 23:397-408(2001).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=21178476; PubMed=11283317;  
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;  
 RT "To eat or to sleep? Orexin in the regulation of feeding and  
 RT wakefulness.";  
 RL Annu. Rev. Neurosci. 24:429-458(2001).  
 RN [4]

RP VARIANT NARCOLEPSY LYS-54, AND MUTAGENESIS OF GLU-54.  
RX MEDLINE=21180003; PubMed=11282968; DOI=10.1101/gr.161001;  
RA Hungs M., Fan J., Lin L., Lin X., Maki R.A., Mignot E.;  
RT "Identification and functional analysis of mutations in the hypocretin  
RT (orexin) genes of narcoleptic canines.";  
RL Genome Res. 11:531-539(2001).  
CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A  
CC and orexin-B neuropeptides.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- DISEASE: Defects in HCRTTR2 are a cause of an autosomal recessive  
CC form of narcolepsy, observed in labradors, dobermans and  
CC dachshunds. Narcolepsy is a neurological sleep disorder affecting  
CC animals and humans, characterized by excessive daytime sleepiness,  
CC sleep fragmentation, symptoms of abnormal rapid-eye-mouvement  
CC (REM) sleep, such as cataplexy, hypnagogic hallucinations, and  
CC sleep paralysis. Cataplexy is a sudden loss of muscle tone  
CC triggered by emotions, which is the most valuable clinical feature  
CC used to diagnose narcolepsy. As in humans, most cases of canine  
CC narcolepsy are sporadic but an autosomal recessive form was also  
CC observed.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF164626; AAD49333.1; -.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR000204; Orexin\_receptor.  
DR InterPro; IPR004060; Orexin\_receptor2.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR Pfam; PF03827; Orexin\_rec2; 1.  
DR PRINTS; PR00237; GPCRRHODOPSN.  
DR PRINTS; PR01522; OREXIN2R.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Disease mutation; G-protein coupled receptor; Glycoprotein;  
KW Transmembrane.  
FT DOMAIN 1 54 Extracellular (Potential).  
FT TRANSMEM 55 75 1 (Potential).  
FT DOMAIN 76 88 Cytoplasmic (Potential).  
FT TRANSMEM 89 110 2 (Potential).  
FT DOMAIN 111 127 Extracellular (Potential).  
FT TRANSMEM 128 150 3 (Potential).  
FT DOMAIN 151 172 Cytoplasmic (Potential).  
FT TRANSMEM 173 193 4 (Potential).  
FT DOMAIN 194 224 Extracellular (Potential).  
FT TRANSMEM 225 247 5 (Potential).  
FT DOMAIN 248 304 Cytoplasmic (Potential).  
FT TRANSMEM 305 327 6 (Potential).  
FT DOMAIN 328 342 Extracellular (Potential).  
FT TRANSMEM 343 366 7 (Potential).  
FT DOMAIN 367 444 Cytoplasmic (Potential).

FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).  
 FT VARIANT 54 54 E -> K (in autosomal recessive narcolepsy).  
 FT MUTAGEN 54 54 E->K: Loss of function.  
 SQ SEQUENCE 444 AA; 50675 MW; D848A4536D485D6B CRC64;  
  
 Query Match 68.1%; Score 1319.5; DB 1; Length 444;  
 Best Local Similarity 71.4%; Pred. No. 1.8e-82;  
 Matches 250; Conservative 42; Mismatches 51; Indels 7; Gaps 3;  
  
 Qy 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYAVFVALVGNTLVCLAVWRNH 75  
 ::|| | ||:| |||||||:||:||:||||| :|:||||| |||:|||:  
 Db 24 TQEPEFLNPTDYDDEEFLRYLWREYLPKEYEWVLIAGYIIVFVALVGNVLVCVAWKNH 83  
  
 Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCKVIPYLQAVSVSVAL 135  
 ||||||| ||| ||| ||| |||:|||:|||:|||:|||:|||:|||:|||:  
 Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFEGQSLCKVIPYLQTVSVSVAL 143  
  
 Qy 136 TLSFIPLDRWYAICHPLLFKSTARARGSILGIWAVSLAIMVPQAAVMQSSVLPPELANR 195  
 ||| | |||||||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNIVIWVSCIIMIPQAIVMECSTMLPGLANK 203  
  
 Qy 196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSALV 255  
 | ||:| ||| :|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVAYLQIFRKWLCRQIPGTSSVVQ 263  
  
 Qy 256 RNWK--RPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLVFALCYLP 313  
 | || :|: | :| :| :| | ||:||:|||:|||:|||:|||:  
 Db 264 RKWKPLQPASQ---PRPGPQQTKSRISAVAAEIKQIRARRKTARMVMVLLVFAICYLP 319  
  
 Qy 314 ISVNLVKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363  
 ||:||||| ||| ||| ||| ||| ||| ||| ||| |||:  
 Db 320 ISIINVLVKRVFGMFTHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369

#### RESULT 8

##### Q6VLX3

ID Q6VLX3 PRELIMINARY; PRT; 443 AA.  
 AC Q6VLX3;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Orexin receptor type-2a.  
 GN Name=MOXR2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Chen J., Randeva H.S.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

DR EMBL; AY339389; AAR11294.1; -.  
 DR EMBL; AY339383; AAR11294.1; JOINED.  
 DR EMBL; AY339384; AAR11294.1; JOINED.  
 DR EMBL; AY339385; AAR11294.1; JOINED.  
 DR EMBL; AY339386; AAR11294.1; JOINED.  
 DR EMBL; AY339387; AAR11294.1; JOINED.  
 DR EMBL; AY339388; AAR11294.1; JOINED.  
 DR EMBL; AY336084; AAR01327.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR000923; BlueCu\_1.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR InterPro; IPR000204; Orexin\_receptor.  
 DR InterPro; IPR004060; Orexin\_receptor2.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR Pfam; PF03827; Orexin\_rec2; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PRINTS; PR01522; OREXIN2R.  
 DR PRINTS; PR01064; OREXINR.  
 DR PROSITE; PS00196; COPPER\_BLUE; UNKNOWN\_1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 67.9%; Score 1315.5; DB 2; Length 443;  
 Best Local Similarity 70.3%; Pred. No. 3.3e-82;  
 Matches 251; Conservative 40; Mismatches 45; Indels 21; Gaps 4;

Qy	17 SREPSPVPPDYED-EFLRYLWRDYLKPQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75 ::       :         :  :  :      :       :      :   :
Db	24 TQEPEFLNPTDYDDEEFLRYLWREYLLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAWKNH 83
Qy	76 HMRTVTNYFIVNLSLADVLVTAICLPASLIVDITESWLFHALCKVIPYLQAVSVSVAL 135                       : :     :     :             :
Db	84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVAL 143
Qy	136 TLSFIPLDRWYAICHPLLKFSTARARRGSILGIWAVSLAIMVPQAAVMQSSSVLPELANR 195              :   :   :      :       :      :   :   :   :
Db	144 TLSCIALDRWYAICHPLMFKSTAKRARNSIVVIWIVSCIIMIPQAIIVMECSSMLPGLANK 203
Qy	196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSAV 255     :        :   :       :   :     :                  :  :
Db	204 TTLFTVCDEHWGGEVYPKMYHICFLVTYMAPLCLMILAYLQIFRKWLCRQIPGTSSVQ 263
Qy	256 RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306     : :  :  :        :  :   :   :
Db	264 RKWKQ-----QQPVSS---QPRGSGQQSKARISAAEIKQIRARRKTARMVMVVLLV 312
Qy	307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363   :     :   :   :                     :   :   :
Db	313 FAICYLPISIILNVLKRVFGMFTHTEDRETIVYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 9

AAR01327

ID AAR01327 PRELIMINARY; PRT; 443 AA.  
AC AAR01327;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Orexin receptor type-2a.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Chen J., Randeva H.S.;  
 RT "Cloning and Characterization of the Mouse Type-2a Orexin Receptor  
 RT Subtype (OX2aR).";  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY336084; AAR01327.1; -.  
 KW Receptor.  
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 67.9%; Score 1315.5; DB 2; Length 443;  
 Best Local Similarity 70.3%; Pred. No. 3.3e-82;  
 Matches 251; Conservative 40; Mismatches 45; Indels 21; Gaps 4;

Qy	17 SREPSPVPPDYED-EFLRYLWRDLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH	75
	::         :          :   :   :        :      :      :   :	
Db	24 TQEPEFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH	83
Qy	76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL	135
	:   :   :     :   :   :   :   :   :	
Db	84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVAL	143
Qy	136 TLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQAAVMQSSSVLPELANR	195
	:   :      :   :      :       :      :       :	
Db	144 TLSCIALDRWYAICHPLMFKSTAKRARNNSIVVIWIVSCIIMIPQAIVMECSSMLPGLANK	203
Qy	196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV	255
	:       :   :      :   :       :       :       :    :  :	
Db	204 TTLFTVCDEHWGGEVYPKMYHICFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQ	263
Qy	256 RNWKRPSDLQGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV	306
	: :  :              :   :   :   :   :	
Db	264 RKWKQ-----QQPVS---QPRGSGQQSKARISAVAEEIKQIRARRKTARMLMVLLV	312
Qy	307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNFLSG	363
	:     :     :               :   :   :   :   :	
Db	313 FAICYLPISILNVLKRVFGMFHTTEDRETVYAWFTFSHLVYANSAANPIIYNFLSG	369

#### RESULT 10

AAR11294

ID AAR11294 PRELIMINARY; PRT; 443 AA.  
 AC AAR11294;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Orexin receptor type-2a.  
 GN MOXR2.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Chen J., Randeva H.S.;  
 RT "Genomic structure analysis of the Mus musculus orexin type-2 (MOXR2) gene."  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY339383; AAR11294.1; JOINED.  
 DR EMBL; AY339384; AAR11294.1; JOINED.  
 DR EMBL; AY339385; AAR11294.1; JOINED.  
 DR EMBL; AY339386; AAR11294.1; JOINED.  
 DR EMBL; AY339387; AAR11294.1; JOINED.  
 DR EMBL; AY339388; AAR11294.1; JOINED.  
 DR EMBL; AY339389; AAR11294.1; -.  
 KW Receptor.  
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 67.9%; Score 1315.5; DB 2; Length 443;  
 Best Local Similarity 70.3%; Pred. No. 3.3e-82;  
 Matches 251; Conservative 40; Mismatches 45; Indels 21; Gaps 4;

Qy	17 SREPSPVPPDYED-EFLRYLWRDYLKPQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH	75
	::       :         :  :  :       :      :     :  :	
Db	24 TQEFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCAVWKNH	83
Qy	76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL	135
	:     :       :   :   :     :     :    :   :	
Db	84 HMRTVTNYFIVNLSLADVLVTITCLPATLVDITETWFFGQSLCKVIPYLQTVSVSVAL	143
Qy	136 TLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAMQSSSVLPELANR	195
	:     :      :      :      :   :	
Db	144 TLSCLIALDRWYAICHPLMFKSTAKRARNNSIVVIWIVSCTIMIPQAIIVMECSSMLPGLANK	203
Qy	196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSALV	255
	:      :   :       :   :     :        :    :   :  :	
Db	204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKWLCRQIPGTSSVVQ	263
Qy	256 RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV	306
	: :  :          :   :   :   :   :	
Db	264 RKWKQ-----QQPVS---QPRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLV	312
Qy	307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNFLSG	363
	:     :     :                 :   :   :   :	
Db	313 FAICYLPISILNVLKRVFGMFTHTEDRETVYAWFTSHWLVYANSAANPIIYNFLSG	369

#### RESULT 11

##### OX2R\_MOUSE

ID OX2R\_MOUSE STANDARD; PRT; 460 AA.  
 AC P58308; Q8BG12;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).  
GN Name=Hcrtr2; Synonyms=Mox2r;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Hypothalamus;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [2]  
RP SEQUENCE OF 100-311 FROM N.A.  
RC STRAIN=C57BL/6;  
RA Szendro P.I., Maevers K., Eichele G.;  
RT "Cloning of mouse orexin receptors.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP REVIEW.  
RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;  
RA Hungs M., Mignot E.;  
RT "Hypocretin/orexin, sleep and narcolepsy.";  
RL Bioessays 23:397-408(2001).  
RN [4]  
RP REVIEW.  
RX MEDLINE=21178476; PubMed=11283317;  
RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;  
RT "To eat or to sleep? Orexin in the regulation of feeding and  
RT wakefulness.";

RL Annu. Rev. Neurosci. 24:429-458(2001).  
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A  
 CC and orexin-B neuropeptides.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AK038551; BAC30039.1; -.  
 DR EMBL; AK048781; BAC33457.1; -.  
 DR EMBL; AF394597; AAK71327.1; -.  
 DR MGD; MGI:1889024; Mox2r.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR000204; Orexin\_receptor.  
 DR InterPro; IPR004060; Orexin\_receptor2.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR Pfam; PF03827; Orexin\_rec2; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PRINTS; PR01522; OREXIN2R.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
 FT DOMAIN 1 54 Extracellular (Potential).  
 FT TRANSMEM 55 75 1 (Potential).  
 FT DOMAIN 76 88 Cytoplasmic (Potential).  
 FT TRANSMEM 89 110 2 (Potential).  
 FT DOMAIN 111 127 Extracellular (Potential).  
 FT TRANSMEM 128 150 3 (Potential).  
 FT DOMAIN 151 172 Cytoplasmic (Potential).  
 FT TRANSMEM 173 193 4 (Potential).  
 FT DOMAIN 194 224 Extracellular (Potential).  
 FT TRANSMEM 225 247 5 (Potential).  
 FT DOMAIN 248 304 Cytoplasmic (Potential).  
 FT TRANSMEM 305 327 6 (Potential).  
 FT DOMAIN 328 342 Extracellular (Potential).  
 FT TRANSMEM 343 366 7 (Potential).  
 FT DOMAIN 367 460 Cytoplasmic (Potential).  
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).  
 FT CONFLICT 201 201 A -> T (in Ref. 2).  
 FT CONFLICT 240 240 I -> V (in Ref. 2).  
 SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

Query Match 67.9%; Score 1315.5; DB 1; Length 460;  
 Best Local Similarity 70.3%; Pred. No. 3.4e-82;  
 Matches 251; Conservative 40; Mismatches 45; Indels 21; Gaps 4;

Qy 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75  
 ::|| | ||:| |||||||:||:||:|||||| |: ||||||:|| ||:||:||:||  
 Db 24 TQEPFLNPTDYDDEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAWKNH 83

Qy            76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCKVIPYLQAVSVSVAL 135  
               ||||||| ||||| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db            84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVAL 143  
               ||| | | | | | | | :| :| :| :| :| :| :| :| :| :| :|  
 Qy            136 TLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQAAMQSSVLPANR 195  
               ||| | | | | | | :| :| :| :| :| :| :| :| :| :| :| :|  
 Db            144 TLSCIALDRWYAICHPLMFKSTAKRARNSIVVIWIVSCIIMIPQAIVMECSSMLPGLANK 203  
               ||| | | | | | | :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy            196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLWGRQIPGTTSALV 255  
               | | | :| | | | :| :| | | | :| :| | | | :| :| :| :| :|  
 Db            204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKWLWCRQIPGTSSVVQ 263  
               ||| | | | | | | :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy            256 RNWKRPQSDQLGDLEQQLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306  
               | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db            264 RKWKQ-----QQPVS---QPRGSGQQSKARIASAVAEEIKQIRARRKTARMLMVLLV 312  
               ||| | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy            307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNFLSG 363  
               ||| :| | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db            313 FAICYLPISILNVLKRVFGMFTHTEDRETYYAWFTFSHLVYANSAANPIIYNFLSG 369  
               ||| | | | | | | | | | | | | | | | | | | | | | | | | | |

## RESULT 12

AAR01328

ID      AAR01328     PRELIMINARY;     PRT;     460 AA.  
 AC      AAR01328;  
 DT      02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT      02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT      02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE      Orexin receptor type-2b.  
 OS      Mus musculus (Mouse).  
 OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX      NCBI\_TaxID=10090;  
 RN      [1]  
 RP      SEQUENCE FROM N.A.  
 RC      STRAIN=BALB/c;  
 RA      Chen J., Randeva H.S.;  
 RT      "Cloning and Characterization of the Mouse Type-2b Orexin Receptor  
         Subtype (OX2bR).";  
 RL      Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 DR      EMBL; AY336085; AAR01328.1; -.  
 KW      Receptor.  
 SQ      SEQUENCE    460 AA;    52461 MW;    D62A67C15BA67DCC CRC64;

Query Match            67.9%;    Score 1315.5;    DB 2;    Length 460;  
 Best Local Similarity    70.3%;    Pred. No. 3.4e-82;  
 Matches    251;    Conservative    40;    Mismatches    45;    Indels    21;    Gaps    4;

Qy            17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75  
               ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db            24 TQEFLNPTDYDDEEFLRYLWREYLPKEYEWVLIAAGYIIVFVVALIGNVLVCVAVWKH 83  
               ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy            76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCKVIPYLQAVSVSVAL 135  
               ||||||| ||||| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db            84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVAL 143

RESULT 13

AAR11293

ID AAR11293 PRELIMINARY; PRT; 460 AA.  
AC AAR11293;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Orexin receptor type-2b.  
GN MOXR2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Chen J., Randeva H.S.;  
RT "Genomic structure analysis of the Mus musculus orexin type-2 (MOXR2) gene.";  
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY339383; AAR11293.1; JOINED.  
DR EMBL; AY339384; AAR11293.1; JOINED.  
DR EMBL; AY339385; AAR11293.1; JOINED.  
DR EMBL; AY339386; AAR11293.1; JOINED.  
DR EMBL; AY339387; AAR11293.1; JOINED.  
DR EMBL; AY339388; AAR11293.1; JOINED.  
DR EMBL; AY339389; AAR11293.1; JOINED.  
DR EMBL; AY339390; AAR11293.1; -.  
KW Receptor.  
SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

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Query Match      67.9%;  Score 1315.5;  DB 2;  Length 460;
Best Local Similarity 70.3%;  Pred. No. 3.4e-82;
Matches 251;  Conservative 40;  Mismatches 45;  Indels 21;  Gaps 4;

Y 17 SREPSPVPPDYED-EFLRYLWRDLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
D    ::||  | ||:| |||||||:||:||:|||:|||  |: ||||||:|| | :||:||:|||
D 24 TQEFLNPTDYDDEEFLRYLWREYLPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKH 83

Y 76 HMRTVTNYFIVNLSADVLVTAICLPA$LLVDITESWLFGHALCKVIPYLQAVSVSVAVL 135

```

|||||||:||||||:||||:||||:|| :||||||:|||:  
 Db 84 HMRTVTNYFIVNLSADVLVTITCLPATLVDVDIRTWFFGQSLCKVIPYLOTVSVSVL 143  
 ||| | |||||:|||:||||:|||:|||:  
 Qy 136 TLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQAAMQSSVLPLEANR 195  
 ||| | |||||:|||:||||:|||:  
 Db 144 TLSCLIALDRWYAICHPLMFKSTAKRARNSIVVIWIVSCIIIMIPQAIVMECSSMLPGLANK 203  
 ||| | |||||:|||:  
 Qy 196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSALV 255  
 ||| | |||:|||:|||:  
 Db 204 TTLFTVCDEHWGGEVYPKMYHICFLVTYMAPLCLMILAYLQIFRKWLRCRQIPGTSSVVQ 263  
 ||| | |||:  
 Qy 256 RNWKRPSDLQLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306  
 ||| | |||:  
 Db 264 RKWQ-----QQPVS---QPRGSGQQSKARISAVAEEIKQIRARRKTARMIMVVLLV 312  
 ||| | |||:  
 Qy 307 FALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363  
 ||| | |||:  
 Db 313 FAICYLPISILNVLKRVFGMFHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369

#### RESULT 14

OX2R\_HUMAN

ID OX2R\_HUMAN STANDARD; PRT; 444 AA.  
 AC O43614;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).  
 GN Name=HCRT2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98150861; PubMed=9491897;  
 RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,  
 RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,  
 RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,  
 RA McNulty D.E., Liu W.-S., Terrell J.A., Elshourbagy N.A., Bergsma D.J.,  
 RA Yanagisawa M.;  
 RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides  
 RT and G protein-coupled receptors that regulate feeding behavior.";  
 RL Cell 92:573-585(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21580342; PubMed=11723285;  
 RA Olafsdottir B.R., Rye D.B., Scammell T.E., Matheson J.K.,  
 RA Stefansson K., Gulcher J.R.;  
 RT "Polymorphisms in hypocretin/orexin pathway genes and narcolepsy.";  
 RL Neurology 57:1896-1899(2001).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;  
 RA Hungs M., Mignot E.;  
 RT "Hypocretin/orexin, sleep and narcolepsy.";  
 RL Bioessays 23:397-408(2001).

RN [4]  
 RP REVIEW.  
 RX MEDLINE=21178476; PubMed=11283317;  
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;  
 RT "To eat or to sleep? Orexin in the regulation of feeding and  
 RT wakefulness.";  
 RL Annu. Rev. Neurosci. 24:429-458(2001).  
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A  
 CC and orexin-B neuropeptides.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -----  
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 CC -----  
 DR EMBL; AF041245; AAC39602.1; -.  
 DR EMBL; AY062031; AAL47215.1; -.  
 DR Genew; HGNC:4849; HCRTR2.  
 DR MIM; 602393; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0008188; F:neuropeptide receptor activity; TAS.  
 DR GO; GO:0007631; P:feeding behavior; TAS.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
 DR GO; GO:0007268; P:synaptic transmission; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR000204; Orexin\_receptor.  
 DR InterPro; IPR004060; Orexin\_receptor2.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR Pfam; PF03827; Orexin\_rec2; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PRINTS; PR01522; OREXIN2R.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
 FT DOMAIN 1 54 Extracellular (Potential).  
 FT TRANSMEM 55 75 1 (Potential).  
 FT DOMAIN 76 88 Cytoplasmic (Potential).  
 FT TRANSMEM 89 110 2 (Potential).  
 FT DOMAIN 111 127 Extracellular (Potential).  
 FT TRANSMEM 128 150 3 (Potential).  
 FT DOMAIN 151 172 Cytoplasmic (Potential).  
 FT TRANSMEM 173 193 4 (Potential).  
 FT DOMAIN 194 224 Extracellular (Potential).  
 FT TRANSMEM 225 247 5 (Potential).  
 FT DOMAIN 248 304 Cytoplasmic (Potential).  
 FT TRANSMEM 305 327 6 (Potential).  
 FT DOMAIN 328 342 Extracellular (Potential).  
 FT TRANSMEM 343 366 7 (Potential).  
 FT DOMAIN 367 444 Cytoplasmic (Potential).  
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).

SQ SEQUENCE 444 AA; 50680 MW; CA0669F0D4224C65 CRC64;  
 Query Match 67.8%; Score 1313.5; DB 1; Length 444;  
 Best Local Similarity 70.0%; Pred. No. 4.6e-82;  
 Matches 250; Conservative 37; Mismatches 49; Indels 21; Gaps 3;  
  
 Qy 17 SREPSPVPPDYED-EFLRLWRDYLYPKQYEWVLIAAYVAVFVALVGNTLVCLAVWRNH 75  
 ::|| | ||:| |||||||:||:||:||||| :| |||||:|| |||:||:||  
 Db 24 TQEPEFLNPTDYEFLRLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCAVWKNH 83  
  
 Qy 76 HMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFHALCKVIPYLQAVSVSVAL 135  
 |||||||:|||||:|||||:|||:|||:|||:|||:|||:|||:|||:  
 Db 84 HMRTVTNYFIVNLSIADVLVTITCLPATLVDITETWFFGQSLCKVIPYLQTVSVSVAL 143  
  
 Qy 136 TLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQAAVMQSSSVLPELANR 195  
 ||| | |||||||:|||||:|||:|||:|||:|||:|||:|||:  
 Db 144 TLSCLIALDRWYAICHPLMFKSTAKRARNISIVIWIVSCIIMIPQAIVMECSTVFPGLANK 203  
  
 Qy 196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSLV 255  
 | ||:|| | ||| :|||:|||:|||:|||:|||:|||:|||:  
 Db 204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKWLWCRQIPGTSSVVQ 263  
  
 Qy 256 RNWKRPSDLQGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306  
 | || | ||| | ||| | |||:|||:|||:|||:|||:  
 Db 264 RKWK-----PLQPVSQPRPGPGQPTKSRMSAVAAEIKQIRARRKTARMLMVLLV 312  
  
 Qy 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363  
 ||:|||||:|||||:|||:  
 Db 313 FAICYLPISILNVLKRVFGMFAHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369

## RESULT 15

AAG28021

ID AAG28021 PRELIMINARY; PRT; 444 AA.  
 AC AAG28021;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypocretin receptor-2.  
 GN HCRT2R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20429525; PubMed=10973318;  
 RA Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,  
 RA Nevsimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,  
 RA Pedrazzoli M., Padigaru M., Kucherlapati M., Fan J., Maki R.,  
 RA Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;  
 RT "A mutation in a case of early onset narcolepsy and a generalized  
 RT absence of hypocretin peptides in human narcoleptic brains.";  
 RL Nat. Med. 6:991-997(2000).  
 DR EMBL; AF202091; AAG28021.1; -.  
 DR EMBL; AF202085; AAG28021.1; JOINED.  
 DR EMBL; AF202086; AAG28021.1; JOINED.

DR EMBL; AF202087; AAG28021.1; JOINED.  
 DR EMBL; AF202088; AAG28021.1; JOINED.  
 DR EMBL; AF202089; AAG28021.1; JOINED.  
 DR EMBL; AF202090; AAG28021.1; JOINED.  
 KW Receptor.  
 SQ SEQUENCE 444 AA; 50680 MW; CA0669F0D4224C65 CRC64;  
  
 Query Match 67.8%; Score 1313.5; DB 2; Length 444;  
 Best Local Similarity 70.0%; Pred. No. 4.6e-82;  
 Matches 250; Conservative 37; Mismatches 49; Indels 21; Gaps 3;  
  
 Qy 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75  
       ::||  |  ||:|  ||||||:||:||:||||||  |:  ||||||:||  |||:|||:|||  
 Db 24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAWWKNH 83  
  
 Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL 135  
       ||||||||||||||||||  ||||:|:||||||:|  ||  :||||||  ||||||:|||  
 Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVDITETWFFGQSLCKVIPYLQTVSVSVAL 143  
  
 Qy 136 TLSFIPLDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQAAMQSSVLPTELAR 195  
       |||  |  |||||||:|||:|||  ||:  ||  ||:|||  ||:  ||  |||:  
 Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNNSIVIIWIVSCIIMIPQAIVMECSTVFPGLANK 203  
  
 Qy 196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSLAV 255  
       |  ||:|  ||  :|  ||:|  ||:|  ||  ||  :|  ||  ||||||  ||||||:|  :  
 Db 204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKLWCRQIPGTSSVQQ 263  
  
 Qy 256 RNWKRPSDLQGDLEQQLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306  
       |  ||                  |  |||                  |  ||:||:|||:|||:|||||||  
 Db 264 RKWK-----PLQPVSQPRGPQOPTKSRSMSAVAEEIKQIRARRKTARMLMVLLV 312  
  
 Qy 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNFLSG 363  
       ||:|||||:|||||||  |||  ||  |||||||  |||||||  |||||||  
 Db 313 FAICYLPISILNVLKRVFGMFAHTEDRETYYAWFTFSHLVYANSAANPIIYNFLSG 369

Search completed: October 14, 2004, 10:55:49  
 Job time : 98.8388 secs